| Novel nucleotide s Coding sequence to Polynucleotide seq Home sapiens 20q13 Human PR0274 nucle Human RNA helicase Coding strand of n Human LOBO homolog C kappa exon prime Plant microsatelli | Human colon cancer Immunogen DNA from Human 5' EST isola Murine Bc1-2 inter Human gene signatu Human secreted pro Murine Bc1-2 inter plant microsatelli Plant microsatelli Plant microsatelli Calcium ion channe Murine Bc1-2 inter EST clone BN180. STreptococcus pneu MAGE-4 encoding ge H6/MAGE-1 expressi | Ho/MacE-1 expressi Homan secreted pro Hepatitis C virus Hepatitis C virus Hepatitis C virus NaNB hepatitis vir CDNA encoding a fo CLYTA-MAGE-1-His f Lipoprotein D-MAGE 16S RNA from ATCC CDNA encoding GTP-b Streptococcus pneu Neurodegenerative Murine D6 encoding Mouse FAST-1 codin Tumour rejection a Human prostate tum Beta(1 -> 4)-N-ace DNA encoding human Human HCDR-1 codin Human HCDR-1 codin Human HCDR-1 codin Human HCDR-1 codin Human HCDR-1 codin Human TRAF four as | E antigen precurso Antigen E gene. H Tumour rejection a MZ2-MEL antigen E Antigen E coding s Tumour rejection a Human melanome ant Human secreted pro Human endometrium Neurodegenerative fdhF gene. Synthe Encodes partial mu T-call surface ant Human CD97 protein Nitrate reductase Xenopus frog prote Sequence of nitrog Human colon carcin Full length expand Human FACC cDNA cl |
|--|--|---|---|
| 8 0.6 1626 20 X0868 8 0.6 2186 19 V1735 8 0.6 2450 20 X2053 8 0.6 2605 19 V0469 8 0.6 2945 20 23389 8 0.6 4120 20 X7035 8 0.6 4999 20 Z2390 7 0.6 226 21 5 G2468 | 6 300 21 A3205 6 300 21 A0138 6 330 21 Z4264 6 332 20 X4499 6 369 20 X4499 6 422 20 X4499 6 422 20 X4499 6 422 20 X4499 6 6 605 6 559 19 V2936 6 6 605 6 6 605 6 791 20 X449 6 1022 20 X449 6 1024 20 X449 6 1024 20 X449 6 1084 20 X449 6 1084 20 Z6446 6 1084 20 Z6446 | 17 0.6 1094 15 067865 17 0.6 1140 20 020441 17 0.6 1140 20 020441 17 0.6 1173 13 029634 17 0.6 1173 14 029634 17 0.6 1173 14 029635 17 0.6 1209 21 246089 17 0.6 1345 12 024459 17 0.6 1345 12 024444 17 0.6 1592 19 042963 17 0.6 1668 20 072116 17 0.6 1668 20 072116 17 0.6 1724 19 038385 17 0.6 1724 19 038385 17 0.6 1816 20 038340 17 0.6 1816 20 038340 17 0.6 1906 21 041550 17 0.6 1906 21 041550 17 0.6 1906 21 041550 17 0.6 1906 21 041550 | 24.18 20 X84.00 0.6 24.19 13 Q2235 0.6 24.19 13 Q2235 0.6 24.19 16 TQ508 0.6 24.19 16 TQ508 0.6 24.20 15 Q7447 0.6 24.20 15 Q7447 0.6 26.20 19 V5595 0.6 2711 9 V6805 0.6 2711 9 V8805 0.6 3156 19 X1847 0.6 3156 19 X1847 0.6 3457 14 Q4086 0.6 4268 18 T4935 0.6 4268 18 T4935 0.6 4488 14 Q5518 0.6 4488 14 Q5518 0.6 4488 14 Q5518 |
| onds codates/sec | 2958 | ************************************** | ption ption colon cancer gene signatu biallelic po biallelic po lella catarha PRO274 hybri gequence fo lori cytoplas colon cancer an inositol 1 lori cytoplas |
| GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. Manucleic - nucleic search, using sw model The companient of the companient of the control of | Jitle: Derfect score: | N_Geneseq_36:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1982.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1983.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1984.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1986.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1986.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1986.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1992.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1993.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT:* Cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT:* | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pri and is derived by analysis of the total score distribution. SUMMARIES Description 1 237 8.0 238 21 280231 Human colo 2 53 1.8 72 16 725953 Human pial 2 53 1.8 68 19 X11554 Human pial 2 4 19 0.6 526 20 V88751 Moraxella 6 18 0.6 177 20 X18066 Coding seq C 7 18 0.6 177 20 X18066 Human PRO2 C 9 18 0.6 531 18 177453 Human colo 10 18 0.6 124812 Human colo 11 18 0.6 1593 18 167992 Human colo |

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| MAGE-1 nucleic aci | Tumour rejection a | MAGE-1 gene. Homo | Lats gene encoding | Drosophila melanog | Tumour rejection a | Arylamine N-acetyl | Streptococcus pneu | Polynucleotide seq | Staphylococcus aur | Rat nestin gene - | Polynucleotide seq | Partial mouse WRN | Complete nucleotid | Human METH1 relate |
|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|
| 032352 | 072477 | X84113 | T42117 | 251508 | 098902 | 048772 | V52165 | X20553 | V74675 | 070447 | X20535 | X83005 | 230163 | 232020 |
| 13 | 15 | 70 | 17 | 21 | 16 | 14 | 19 | 20 | 18 | 15 | 50 | 18 | 20 | 20 |
| 5674 | 5674 | 5674 | 5720 | 5720 | 5724 | 6464 | 10240 | 10461 | 10813 | 11236 | 21170 | 29604 | 34094 | 38734 |
| 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 9.0 | 0.6 |
| 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 | 17 |
| 98 | 87 | 88 | 88 | 06 | 91 | 92 | 63 | 94 | 95 | 96 | 2 97 | 86 | 66 | 2 100 |

ALIGNMENTS

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SSULT
30231
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Z80231 standard; cDNA; 238 BP

280231;

(first entry) 07-APR-2000

Human colon cancer cell line SW480 cDNA clone SEQ ID NO:315.

Human; gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytoStatic; sarcoma; breast cancer; neoplasia; dysplasia; hyperplasia; ds.

Homo sapiens

W09964576-A2 16-DEC-1999 99WO-IB01062 09-JUN-1999; 98US-0088801 10-JUN-1998;

(FARB) BAYER CORP.

Monahan JE; I, Astle JH, Burgess CC, Bushnell Derti A, Ford DM, Lewis ME, Monah Steinmann KE, Catino TJ, D Endege WO, Carroll E, Schlegel R;

WPI; 2000-087220/07

Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer

Claim 15; Page 258; 469pp; English.

Another than the color cancer is soluted from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The human colorectal adenocarcinoma (colon cancer) cell line SW480. The canba clones can be used to generate antisense oligonucleocides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders; involving unwanted cell proliferation, such as neoplasia, dysplasia or hyperplasia

Sequence 238 BP; 55 A; 57 C; 69 G; 57 T; 0 other;

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double-stranded DNA, which comprises one of the 7837 "GS" sequences given in T19001-T2687 and which is able to hybridise to part of human genomic DNA, which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(7) as the sole primer. Since the 3'-confined cDNA by using poly(7) as the sole primer. Since the 3'-confined cDNA hybridise with specific mRNAs. Each library is confirtucted so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS. sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                  226 acctgcaggtggtggcagcgggtagccgggactcgggcgccgcgctctacgtcttctccg 285
                                                                                                                                                                                                    405
                                                                                                                                                                                                                                   121 agttaaaggttgctcgcctggacaacatattcctgacacgaatgcactggtctaatgttg 180
                                  Gaps
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                                                                                                                                                                                                                                                                agttaaaggttgctcgcctggacaacatattcctgacacgaatgcactggtctaatgttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                  ö
Length 238,
                                  Indels
                 4.1e-106;
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 DB 21;
8.0%; Score 237; DE 100.0%; Pred. No. 4.1 iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     T25953 standard; cDNA to mRNA; 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene signature HUMGS08188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-OCT-1996 (first entry)
 Query Match 8.0°
Best Local Similarity 100.
Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-206931/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                       T25953;
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                                                                                                                                                                                                                                                                                                                                                       RESULT
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Length 68;

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Seguence 72 BP; 25 A; 10 C; 16 G; 20 T; 1 other;

recognising different cell types.

8×3

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X10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in X09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Adrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, hereditary shaemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic or encophisms of such diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
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                                                                                            Length 72;
                                                        Indels
         DB 16; Le
4.4e-16;
hes 0;
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             1.8%; Score 53; DB 100.0%; Pred. No. 4.4 Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                        Conservative
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X11554 standard; DNA; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment; marker; ss.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating, preventing or ameliozating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic.activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for
                                                                                                                                                                                                                                                                                                               Expressed sequence tag; secreted protein; haematopoiesis regulator; issue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostaxis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                          Gaps
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                                         Indels
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      DB 19; I
3.1e-09;
                                                                          tggaaacagacggcgcacctttcctctaatccagcaaa 2850
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                                                                                          62 TGGAAACAGACGGCGCACTTTCCTCTAATCCAGCAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity. The EST sequences are also stated to
1.3%; Scor.
100.0%; Pred. No. 5.-
... 0; Mismatches
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100.0%; Pred. No. 18;
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Treacy M;
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                                                                                                                                                                                     V88751 standard; cDNA; 526
                                                                                                                                                                                                                                                  12-FEB-1999 (first entry)
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                                          Conservative
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agostino MJ, Jacobs K,
Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070078/06.
                            Similarity
                                                                                                                                                                                                                                                                                  EST clone HK189
      Query Match
Best Local Simi
Matches 39;
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Sequence 68 BP; 12 A; 13 C; 21 G; 21 T; 1 other;

such diseases

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P-PSDB; W89417, W89418, W89419, W89420
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98US-0077649.
98US-0077791.
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98US-0078886.
98US-0078910.
98US-0078936.
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                                                                                                                                                                                                                                                      the lower respiratory
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Matches 19; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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11-MAR-1998;
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                                                   infections
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   δλ
                                                                                                                                                                                                                                                                                                    /transl_except= (pos:509..512, aa:Asp)
/note= "this codon has an apparent 1 codon
insertion, which alters the reading frame"
/note= "lbpB is specifically claimed in Claim 8;
encodes W89417"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tog= i
/*tog= lbpA
/product= lbpA
/note= "specifically claimed in claim 8; encodes
//note= "W89419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene- orf3
/note- "specifically claimed in Claim 7; encodes
W89419"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /product=^LBP1
/note= "specifically claimed in Claim 8; encodes
w89418"
                                                                                                                     Lactoferrin receptor; lactoferrin binding protein; LBP1; LBP2; lbpA gene; lbpB gene; ORF3; infection; otifits media: sinusitis; conjunctivitis; pneumonia; bronchitis; tracheitis; anhysema; diagnosis; therapy; vaccine; Branhamella caturrhalis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang Q,
                                                                                                   Moraxella catarrhalis Q8 lfr region.
                                                                                                                                                                                            Location/Qualifiers 90..95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Du R, Klein MH, Loosmore SM,
                                                                                                                                                                                                                                                                                              'product- LBP2
                                        V82020 standard; DNA; 7642 BP
                                                                                                                                                                                                                       108..113
/*tag= b
138..147
/*tag= c
/*tag= c
/*tag= d
/*tag= d
/*tag= d
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/*tag= r
/22
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97US-0867941.
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/gene= lbpA
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2991..2996
                                                                                21-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                      2974..2979
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                                                                                                                                                                                                                /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                         Moraxella catarrhalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070266/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9855606-A2
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03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1998.
                                                                                                                                                                                           Key
-35_signal
                                                                                                                                                                                                                        -10_signal
                                                                                                                                                                                                                                                                                                                                                                          -10_signal
                                                                                                                                                                                                                                                                                                                                                        -35_signal
                                                            V82020;
                                                                                                                                                                                                                                                                                                                                                                                               RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                             RBS
                             .32020
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This polynucleotide comprises the lactoferrin receptor (lfr) locus of Moraxella catarrhalis (Branhamella catarrhalis) Q8. There are 3 tandem genes in locus, identified as lbpA, lbpB (alternative start codons) and orf3A, respectively encoding lactoferrin binding protein 2 (lbp2, see W89417), lactoferrin binding protein 1 (lbp1, see W89418) and open reading frame protein 3 (ORF3, see W89418 and W89419) and open reading frame protein 3 (ORF3, see W89418 train Q8 genomic DNA library and screening with catarrhalis strain Q8 genomic DNA library and screening with specific hybridisation probes. The genes and DNA sequences of the 1fr locus are useful for diagnosis, immunisation, and the generation of diagnostic and immunological reagents. Immunogenic compositions, including vaccines, based upon expressed recombinant compositions, including vaccines, based upon expressed recombinant compositions of diseases caused by Moraxella. M. catarrhalis is a causative agent of cittis media and has been associated with sinusitis, conjunctivitis and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Lactoferrin receptor genes from Moraxella, especially M. catarrhalis - useful to diagnose Moraxella infection e.g. to detect otitis media due to M. catarrhalis infection and to immunise against such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tract, such as pneumonia, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7642 BP; 2417 A; 1726 C; 1631 G; 1868 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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100.0%; Pred. No. 18;
iive 0; Mismatches
                                                                                                                                                                                                                                                    Claim 8; Fig 4A-4P'; 202pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO274 hybridisation probe.
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98US-0084366.
98US-0084414.
98US-0084441.
98US-0079920
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98US-00846
98US-00846
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980S-0(
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                                                                 0-SD86
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. 233891 to 234338, and Y41685 to Y41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D2H; hPEPT1; human; GI tract receptor; sucrose-isomaltase complex; intestinal peptide-associated transporter; hypertension; diabetes; osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;
                                                                                                                                                                                                        New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                       Chen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 45;
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                                                                                                                                         Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coding sequence for human SI binding protein SNi45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 other;
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Pred. No. 60;
0; Mismatches
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, Singleton J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic agent delivery; therapy; ss
                                                                                                                                         Yuan
                                                                                                                                                                                                                                                                                 Example 4; Page 184; 530pp; English.
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100.0%; Pr
                                                                                                                                         Gurney A,
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                                98US-0087208.
98US-0094651.
98US-0100038.
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Patterson CA,
98US-0087098
98US-0087106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CYTO-) CYTOGEN CORP. (ELAN-) ELAN CORP PLC.
                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                         Goddard A,
                                                                                                                                                                        WPI; 1999-551358/46.
                                                                                                                                                                                                                                            adhesion disorders
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Omahony DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                  28-MAY-1998;
30-JUL-1998;
 28-MAY-1998)
28-MAY-1998)
                                                                    11-SEP-1998
                                                                                                                                       Wood WI,
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acid sequences and related vaccines to treat or prevent H. pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: This DNA sequence is not reproduced in the specification and has been derived from the related specification, W09719098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunisation; detection; antisense; inhibition; cytoplasmic; Na+/H+ antiporter; Escherichia coli; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a Helicobacter pylori cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 18; DB 18; Length 531;
00.0%; Pred. No. 57;
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/transl_except= (pos: 520..522,
/transl_except= (pos: 526..528,
/note= "xaa = unknown"
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                                                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences
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                                                                                                      Mellgaerd BL;
                                                                                                                                                                                                                                                                polypeptide(s) - useful for vaccines
infection, and to detect Helicobacter
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1..531
                                                                                                                                                                                                                                                                                                                                        Claim 9; Page -; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prt
0;
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95US-0487032
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                                                                                                        Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori.
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Matches 18; Conserve
                                                                                                                                                       WPI; 1997-052306/05
                                                    (ASTR ) ASTRA AB.
                                                                                                                                                                                        P-PSDB; W20335.
                                                                                                        Berglindh OT,
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9719098-A1
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T77453/c
This sequence encodes a peptide that specifically binds to the human sucrose-isomaltase complex. The invention relates to purified proteins (I) that bind specifically to at least one of the gastro-intestinal (GI) tract receptors human intestinal associated transporter (HPTI), hPEPTI, DZH and human peptide-associated transporter (HPTI), hPEPTI, DZH and human sucrose-isomaltase complex (HSI). (I) provide active transport of therapeutic agents through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, migrathe, or angina pectoris. Specifically they are used to deliver insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antigens. (I) may also provide targeting to the GI tract. Other uses of (I) ane (I) and (I) in a binding assay); and (ii) to screen for molecules that bind (I) manance of in immunogenic analogues or derivatives of (I) are used to raise antibodies and in immunosasys. The antibodies are used to locate, detect and masser of the level of are used to locate, detect and masser of the level of are used to raise antibodies.
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                                                 New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras and antibodies, used to deliver therapeutic or diagnostic agents to, or through, the gastrointestinal tract, e.g. insulin or leuprolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; prevention; treatment; infection; identification;
binding compound; bacterium; life cycle; activator; bacteria;
inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           measure (I), e.g. for imaging, monitoring treatment, tietc., also for peptide purification and immobilisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 177 BP; 31 A; 51 C; 53 G; 42 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_except= (pos: 460..462,
/transl_except= (pos: 520..522,
/transl_except= (pos: 526..528,
/note= "xaa = Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori cytoplasmic protein ORF 24824087.aa.
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                                                                                                                                                                                        Claim 49; Page 56; 294pp; English
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/note= "Xaa = Un.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1816 agcagtaccacaaccagt 1833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 AGCAGTACCACAACCAGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori.
WPI; 1999-009568/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytoplasmic; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9640893-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996
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T67773;

192885225548838220

Gaps

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Indels

WPI; 1997-298052/27.

P-PSDB; W24635

(ASTR) ASTRA AB.

Smith DH;

17-NOV-1995;

15-NOV-1996; 29-MAY-1997

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279917 to 280766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia, dysplasia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inositol 1,3,4-triphosphate 5/6-kinase; phytic acid; genetic mapping;
myo-inositol 1,2,3,4,5,6-hexaphosphate; biosynthetic enzyme; phytate;
                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
                                                                                                                                                                                                                                        Astle JH, Burgess CC, Bushnell SE;
rti A, Ford DM, Lewis ME, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soybean inositol 1,3,4-triphosphate 5/6-kinase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 21; Length 726;
Pred. No. 57;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 726 BP; 149 A; 157 C; 170 G; 198 T; 52 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DUPO') DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 462; 469pp; English.
                                                                                                                                                                                                                                                                 Derti A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; SCO.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248812 standard; cDNA; 1040 BP.
                                                                           99WO-IB01062.
                                                                                                                                98US-0088801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 cctgcaggtggtggcagc 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    067802U-0W66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 cctgcaggtggtggcage 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000 (first entry)
                                                                                                                                                                                                                                        Steinmann KE,
Catino TJ, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.6
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-087220/07.
                                                                                                                                                                                     (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animal feed; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9955879-A1
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                                                                           09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1999.
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                                                                                                                                10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max.
                      16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperplasia
                                                                                                                                                                                                                                                                   Carroll E,
Schlegel R;
                                                                                                                                                                                                                                        Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248812
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. Pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. Pylori or locates sequence. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. Pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. Pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique Betzt.linker adapters in 100-1000 fold molar excess. These linkers are complementary to the Batzi-cut pMPX vectors, will ethe overhang is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linker-adapter inserts were ligated to each of the 20 pMFX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia; hyperplasia; ds.
                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori nucleic acid sequences and related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a Helicobacter pylori cytoplasmic protein, which was found to be homologous to Escherichia coli Na+/H+ antiporter protein following BLAST protein analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The ORF/protein reference number for this sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer cell line SW480 cDNA clone SEQ ID NO:833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ore 18; DB 18; Length 531;
red. No. 57;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 531 BP; 175 A; 88 C; 114 G; 151 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           obtained from the related specification, WO9640893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                        used for diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 100; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%; So
Best Local Similarity 100.0%; P.
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280749 standard; cDNA; 726 BP
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                                                  96WO-US18542
                                                                                                       95US-0561469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 AAAGCCGCTTCACCCTTT 294
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Note:

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Gaps

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Pearlstein RW;

Hitz WD,

Carlson TJ,

Cahoon RE,

Homo sapiens W09964576-A2

07-APR-2000

Z80749;

ESULT 10 30749

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WPI; 2000-072179/06

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protein of the invention. TIX is a phytic acid (Myc-inostic) the invention. TIX is a phytic acid (Myc-inostic) to protein of the invention. TIX is a phytic acid (Myc-inostic) in 2,3,4,5,6-hexaphosphate) biosynthetic enzyme. The ITX enzymes of the invention may be prepared recombinantly and used to raise antibodies, which are used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides of the invention may be used to reacte transgenic plants in which the ITX levels are present at higher or lower levels than normally ound. This would alter the level of where they are not normally found. This would alter the level of 1,3,4-triphosphate 5/6 knase found in those cells. In addition, it may be desirable to eliminate expression of ITX genes for certain applications. The polynucleotides also serve as a source of probes and applications. The polynucleotides also serve as a source of probes and applications. The physical mapping. Decreased amounts of phytate species, as well as for physical mapping. Decreased amounts of phytate and increased amounts of available phosphate in animal feeds such as corn would lead to improved feed efficiency. The proteins of the present invention lead to a better understanding of the phytic acid biosynthesis pathway, allowing it to be exploited for commercial uses, e.g. in animal
                                                     Novel phytic acid biosynthetic enzymes used to alter the level of the
                                                                                                                                                                                                            This sequence encodes an inositol 1,3,4-triphosphate 5/6-kinase (ITK)
                                                                                                                                                63pp; English.
                                                                                        enzyme in transgenic plants
                                                                                                                                                   Claim 2; Page 53;
P-PSDB; Y59428
KYRRKWKOOOCOOOOOOOOOOOO
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Sequence 1040 BP; 264 A; 255 C; 265 G; 256 T; 0 other;

Gaps ö 21; Length 1040; Indels .; 0 Score 18; DB Pred. No. 56; Mismatches 0.6%; Scilarity 100.0%; P 990 gaaagcttcattcaaccc 1007 Local Similarity hes 18; Conserv Query Match Best Local S Matches 18

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67992/c :> T67992 standard; DNA; 1593 BP. T67992; SULT 12 URCKERMESESEANNAUL

H. pylori cytoplasmic protein ORF 06cp30603orf11. 16-JUL-1997 (first entry)

Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; ds

Helicobacter pylori.

/*tag= a /note= "no stop codon given" Location/Qualifiers 1..1593

WO9640893-A1 19-DEC-1996 96WO-US09122 96US-0630405. 95US-0487032. 06-JUN-1996; 01-APR-1996; 07-JUN-1995;

(ASTR) ASTRA

Treacy M;

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The present sequence encodes a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or trast H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To dientify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                    polypeptide(s) - useful for vaccines to treat or prevent H. pyloriinfection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide; protein; nutrition; cytokine; cell proliferation; cell differentiation; immunostimulation; immunosuppression; haematopoiesis regulation; tissue growth; activin; inhibin; chemotaxis; chemotaxis; haemostasis; thrombolysis; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligand; anti-inflammatory; tumour suppression; gene therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleotide sequence encoding new protein (Clone AC222_1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1593 BP; 541 A; 288 C; 334 G; 430 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R, Evans C, Jacobs K, I
Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 18; DB
.00.0%; Pred. No. 56;
.ve 0; Mismatches
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/product= "Novel protein"
Smith D, Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
161..1129
                                                                                                                                               Claim 9; Page 833; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.00,
100.0%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1760 aaagccgcttcacccttt 1777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agostino MJ, Bowman M
McCoy JM, Merberg D,
                             WPI; 1997-052306/05
Berglindh OT,
                                              P-PSDB; W20739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-APR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X08683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
X08683/c
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Gaps

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Gaps

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Indels

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Length 2186;

19;

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the invention (the encoded protein is not given in the specification). The inhibitor is a Kexz proteinase family enzyme inhibitor with a molecular weight of 11.500. The inhibitor/protein (termed Kexstatin) is expected to have pharmaceutical and pesticidal applications.
                                            sequence is the coding sequence for an example of the inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X20500-21243 represent polynucleotide sequences from the genome of
Treponema pallidum. The sequences can be used for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2450 BP; 553 A; 643 C; 631 G; 617 T; 6 other;
                                                                                                                                                                                    Sequence 2186 BP; 297 A; 827 C; 780 G; 282 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of biosynthetic products such as enzymes
                                                                                                                                                                                                                                                         Score 18; DB 1
Pred. No. 55;
0; Mismatches
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Pred. No. 55;
0; Mismatches
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Disclosure; Page 18-19; 29pp; English.
                                                                                                                                                                                                                                            0.6%; Scor
100.0%; Pre
0;
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                         1652 ggtcctgggcacctggc 1669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X20537 standard; DNA; 2450
                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 18; Conserv
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8 X C C C C C X S
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                                                                                                                                                                                 The new human secreted proteins are encoded by polynucleotides obtained from human placenta, adult testes, fetal kidney, fetal brain, adult brain and adult blood cDNA libraries. The polynucleotides and proteins are predicted to have blological activities which would make them suitable for treating, preventing or amellorating medical conditions in humans and animals. Suggested
                                                                                                                                                                                                                                                                                                                           activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, immune stimulating (e.g. as activity, tissue growth activity, activity, negliating activity, tesue growth activity, activity, activity, activity, activity, activity, activity, activity, activity, and thrombolytic activity. The polymucieotides are also stated to be useful for generally. The sequences are identified by a secretory leader sequence motif in the polymucleotide and it is thought that the encoded proteins have biological activity by virtue of their secreted mature. This clone was designated AC222_1. A probe for this clone is described in x08698.
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pesticidal applications
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                                                                                             New polynucleotides encoding secreted human proteins
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56;
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Pred. No.
                                                                                                                                       Claim 14; Page 101-102; 136pp; English.
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100.0%; Pre
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96JP-0158677.
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Best Local Similarity
Matches 18; Conserv
                                            P-PSDB; W85718
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19-JUN-1996;
26-AUG-1996;
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Gaps

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Length 2450; Indels

Homo sapiens WO9802539-A1

V04699;

ESULT 16 104699/c

15-JUL-1997;

22-JAN-1998

15-JUL-1996; 16-OCT-1996; 17-JAN-1997;

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Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                                         Human PRO274 nucleotides sequence.
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98US-0081070.
98US-0081071.
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98US-0083392.
98US-0083495.
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98US-0082700
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98US-0080194
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98US-0080334
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98US-0081955
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                                          (first entry)
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98US-0081
98US-0081
                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                  W09946281-A2.
                                          07-DEC-1999
                                                                                                                                                                                                                                                              08-MAR-1999;
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           Z33895;
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                                                                                                                                                                   20q13 amplicon; chromosome 20; tumour; detection; chromosomal abnormalities; probe; gene therapy; antisense inhibition; treatment; age-related macular degeneration; retinitis pigmentation; Leber's congenital amaurosis; ds.
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100.0%; Pred. No. 55;
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Rommens J;
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                                                                                                                                       Homo sapiens 20q13 amplicon cc43 transcript.
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Best Local Similarity, 100.0%; P.
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33895
2 233895 standard; cDNA; 2945 BP.
                                            V04699 standard; cDNA; 2605 BP
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96US-0680395.
96US-0731499.
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98US-0083545 98US-0083554

pigmentation.

(first entry)

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This invention describes the construction of a novel insect cell vector (A) which contains a nucleic acid (I) that codes for a protein (II) of the DRAD-superfamily. (A), and recombinant insect viruses derived from them, are used to express recombinant (II), particularly RNA and DNA helicases. (II) are potentially useful for: (a) production of cell lines for research into cancer, inflammation and apoptosis, or for clarifying the mechanism of action of drugs, and (b) to identify pharmaceutical activity in known compounds, e.g. anticancer and antiviral activities. (II), which are difficult to express in bacteria and yeast, are expressed at high lavel in insect cells, e.g. 300-400 mg per 109 cells. This sequence encodes a human RNA-helicase pl35 protein which is used in the description of the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New insect cell vector containing the sequence encoding a DEAD-superfamily protein, particularly a nucleic acid helicase, used e.g. for identifying potential pharmaceuticals
                                                                                                                                                    DEAD protein; insect cell vector; DEAD-superfamily; RNA helicase; DNA helicase; cancer research; cell line; inflammation; apoptosis; drug; anticancer; antiviral; p135; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 38-40; 43pp; German
                                                                                                                     Human RNA helicase p135 DNA #2.
  Z09473 standard; DNA; 4120 BP.
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                                                                                                                                                                                                                                         Homo sapiens
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Matches
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V70354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes secreted and transmembrane polypeptides and their polynuclectides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion, disorders. They may also be used to raise antibodies. x233891 to '234338, and Y41685 to Y41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention.
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                                                         98US-0084414.
98US-0084414.
98US-0084441.
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P-PSDB; Y41686.
29-APR-1998;
29-APR-1998;
30-APR-1998;
05-MAY-1998;
                                                                            06-MAY-1998;
06-MAY-1998;
07-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood WI,
                                                                                                                                                                                                                                                                                                                                                            MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                    MAY-1
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Gallert K, Huels C, Muellner S;

99WO-EP00829. 98DE-1005781.

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Gaps
                                                                                                                                                                                                                                                                                                 Prostate cancer; detection; hK2; hK1; hK3; phK2; tissue kallikrein; pphK2; prostate-specific glandular kallikrein protein; PSA; human; prostate-specific antigen; ss.
                                                                  ö
                                         20; Length 4120;
Sequence 4120 BP; 1099 A; 1021 C; 1236 G; 764 T; 0 other;
                                                                 0; Indels
                                      DB .
                                                                    Mismatches
                                         Score 18;
Pred. No.
                                                                                                                                                                                                                                                                         Coding strand of native genomic hK2.
                                         0.00.
100.08; Pr.
0;
                                                                                                                                                                                           V70354 standard; DNA; 6139 BP.
                                                                                            1338 aggagggagtggcagagg 1355
                                                                                                                       809 AGGAGGGAGTGGCAGAGG 792
                                                                                                                                                                                                                                               (first entry)
                                                    Local Similarity 100.
nes 18; Conservative
                                                                                                                                                                                                                                       09-FEB-1999
                                                                                                                                                                                                                    V70354;
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· . 0

Gaps

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0; Indels

0.6%; Score 18; DB 20; 100.0%; Pred. No. 55; tive 0; Mismatches 0

2; .0

18; Conservative

Best Local Similarity

Matches

Query Match

Length 2945;

Wirth T;

Aigner T,

us-09-434-382-3.olig.rng

Homo sapiens

WO9846795-A1

22-OCT-1998

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bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic, are useful for production of transgenic animals, especially a transgenic, e.g. spondyloepiphysal dysplasia and achodroplasia. This sequence encodes a human LOBO protein described
                                                                                                                                                                            novel nucleic acids (I; designated LOBO (long
                                                                          proteins which influence bone development.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49999 BP; 10983 A; 13723 C; 13439 G; 11854 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    implantation, esp. for prodn. of humanised antibodies in mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homologous replacement of gene in mammalian germ line - by transfecting embryonic stem cell with labelled recombination wehicle, selection and incorporating into blastocyst(s) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Germ line; stem cell; blastocyst; implantation; embryonic;
electroporation; kappa; constant; exon; ss.
                                                                                               useful for treating and studying bone disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 2
Pred. No. 52;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOERDERUNG IMMUNOLOGIE
                                                                                                                                    Example 3; Page 328-356; 391pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Scc...
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                          in the method of the invention.
Hess J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Column 4; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 14820 GGGCCAGGAGGCTGCCAC 14803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2740 gggccaggaggctgccac 2757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92DE-4228162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q54684 standard; DNA; 21
                                                                          acids encoding
Rosenthal A, Rump A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RAJE/) RAJEWSKY K. (KOEL-) KOELNER VER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-008862/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C kappa exon primer.
                                   WPI; 1999-601320/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ses 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zon Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                          Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     054684;
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Matches
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Q54684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kallfxrein 2 (hKZ) DNN. The method comprises: (a) contacting DNA obtained by reverse transcription (RT) of RNA from a human physiological sample by reverse transcription (RT) of RNA from a human physiological sample by reverse transcription (RT) of RNA from a human physiological sample obligionuclectides to amplify the DNA by PCR to yield amplified hKZ DNA, where the conditions amplify the DNA obtained by RT of RNA from at least one cells; and (b) detecting the presence of the amplified hKZ DNA. The method can be used for detecting, monitoring the progression of and pathologically staging prostate cancer. The present sequence represents the coding strand of native genomic hKZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a diagnostic method for detecting human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                 Detection of human kallikrein 2 RNA - by reverse transcription and amplification by PCR, for detecting, monitoring and staging of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 19; Length 6139;
Pred. No. 54;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6139 BP; 1233 A; 1875 C; 1595 G; 1436 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human LOBO homologue genomic DNA fragment 5.
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 78-80; 90pp; English.
                                                                                                                                                                                                                                                        Young CYF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.00,
100.08; Pre
                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3/c
223903 standard; DNA; 49999 BP.
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                                                                                                                  98WO-US07027
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nes 18; Conservative
                                                                                                                                                                                                                                                      Slawin KM, Tindall DJ,
                                                                                                                                                                                                                 (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                                            WPI; 1998-594592/50
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Query Match Best Local S

Matches

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DSM 7211 is made by (1) inserting a fragment of pC:2 (contg. the C kappa exon) into pT2-19(R); (2) inserting a 1.2 kb fragment of pHBc kappa (contg. the intron enhancer element);

98DE-1013799

26-MAR-1999; 27-MAR-1998;

07-OCT-1999.

Homo sapiens.

Z23903;

20

SSULT : 23903, W09950284-A2

(ROSE/) ROSENTHAL A.

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Gaps

; 0

Indels

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Length 49999;

20;

prostate cancer

11-APR-1997;

09-APR-1998;

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Length 256;

35 G; 91 T; 0 other;

89 A; 41 C;

Sequence 256 BP;

XX OS

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Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant microsatellite markers and associated flanking species for detection of polymorphic genetic markers \mbox{-}
                                                                                  codon of this exon.

DSM 7211 was introduced into embryonic mouse stem cells by electroporation. Wild type mice have in their serum no antibodies carrying the human kappa gene constant region, but in mice homozygotic for the mutation, such antibodies were present at
(3) inserting a 1.1 kb fragment contg. the neomycin resistance gene of pMCIneo; (4) inserting the 2.8 kb fragment of pHJKappa (contg. the J1-5) elements); then (5) finally inserting a 427 bp fragment made by PCR on mouse germ line DNA using one primer (Q54683) which hybridises 12 bp after the start of the C kappa exon and another (Q54684) which hybridises 137 bp after the stop
                                                                                                                                                                                                 0.6%; Score 17; DB 15; Lengu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
(FLET-) FLETCHER CHALLENGE FORESIS LTD.
                                                                                                                                                                                      Sequence 21 BP; 8 A; 2 C; 10 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bloksberg LN, Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant microsatellite marker #1040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 382; 392pp; English.
                                                                                                                                                                                                                                0.00,
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                       45SULT 22
-32079/c
:D A32079 standard; DNA; 256 BP.
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                                                                                                                                                                                                                                                                                      1031 gaggtaccaaggaaagg 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-116958/10.
                                                                                                                                                                                                                                            Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Havukkala IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09967421-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1998;
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Gaps

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Sequences A31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences A32094-A32096 with left and right flanking sequences. The polynuclectide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonuclectide fingerprinting and library screening and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant microsatellite sequence; core repeat sequence; detection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New plant microsatellite markers and associated flanking species for
the detection of polymorphic genetic markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful to locate specific economically useful genes in plant genomes
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
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100.0%; Pred. No. 1.8e+02; 
iive 0; Mismatches 0; Indels
                                                                                              Indels
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                           Score 17; DB 21; I
Pred. No. 1.8e+02;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FLET-) FLETCHER CHALLENGE FORESTS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 373; 392pp; English.
0.6%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant microsatellite marker #1011
                                                                                                                                                                                                                                                                                                                                                            A32050/c
ID A32050 standard; DNA; 300 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-NZ00092.
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                                                                                                                                                         2021 tggctggaaagtggtct 2037
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Matches 17; Conservative
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-116958/10.
                           Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Havukkala IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pinus radiata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A32050;
                                                                                                                                                                                                                                                                                                                                    RESULT 23
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and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences A32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluations of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes.

Sequences A31040-A32093 represent novel plant microsatellite sequences

A01382 standard; cDNA; 300 BP

.SSULT 24

19-MAY-2000 (first entry)

A01382;

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0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New non-A, -B, -C, -D and -E (n-(ABCDE)) hepatitis DNA libraries - used to develop prods. for the detection, diagnosis, prevention and treatment of n-(ABCDE) hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide associated with non-A, non-B, non-C, non-D, non-E hepatitis virus (n-(ABCDE) virus) infection, and is obtained by preparing a phage from a phage lambda gill library of MY 190 DNA (ATCC 75284) n-(ABCDE) hepatitis serum, plating to form plaques, and screening the phage plaques for the production of polypeptides immunoreactive with n-(ABCDE) serum n-(ABCDE) hepatitis virus polypeptides can be used for the production or detection of antibodies, and in vaccines. The antibodies can be used for detection, diagnosis and in passive immunotherapy. The DNA can also be used in detection and diagnosis, and as hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes for identification of further n-(ABCDE) hepatitis coding sequences. Culture systems producing the n-(ABCDE) polypeptides can be used in screening studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-A, non-B, non-C, non-D, non-E hepatitis virus MY 190 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents clone D30 which encodes an immunogenic
                                                                                                                                                                                                                                                                                                                                                   non-D, non-E hepatitis virus; n-(ABCDE); vaccine; phage library; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 304;
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Pred. No. 1.8e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 304 BP; 65, A; 93 C; 94 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                                    Immunogen DNA from n-(ABCDE) hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENELABS TECHNOLOGIES INC.
US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 101; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Scc.
100.0%; Pre
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                                                                  T07238 standard; DNA; 304 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US05980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0246986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 cecceceAececece
                                                                                                                                                                                                                                                                                                                                                       Non-A, non-B, non-C,
immunogen; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim JP, Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-020585/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9532290-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2000
                                                                                                                                                                                                                  05-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE-)
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                                                                                                                                            T07238;
RESULT 25
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242643/c
                                 r07238/c
                                                                                                           NAME OF THE PROOF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated on the cell from which the test sample was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sudduth-Klinger J;
Pot D, Kassam A;
                                                                                                                                                                                                                                                Human colon cancer cell line polynucleotide sequence SEQ ID NO:1373.
                                                                                                                                                                                                                                                                                                                  Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
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Randazzo F, Kennedy GC, Pot D, Kassan
CIkveson M, Dickson M, Drmanac S,
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 17; DB 21; Length*300;.
100.0%; Pred. No. 1.8e+02;
.ve 0; Mismatches 0; Indels (
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Claim 1; Page 511; 1097pp; English.

cells

98US-0085537 98US-0085696

98US-0105234 98US-0105877

21-0CT-1998 27-0CT-1998 15-MAY-1998 15-MAY-1998

Escobedo J,

(CHIR) CHIRON CORP. (HYSE-) HYSEQ INC.

s LT, Escard, C, Giese K,

Williams LT, Reinhard C,

ŎĸŀŔijĸŖĸĸŔĸĸĸĸĸŨĸŀĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸŊij

Lamson G,

Leshkowitz D, Kita D, Drmanac R,

WPI; 2000-126369/11.

99WO-US10602 98US-0085426

13-MAY-1999; 18-NOV-1999.

14-MAY-1998

W09958675-A2 Homo sapiens

ö

negative breast cancer, lung cancer, and colon cancer Sequence 300 BP; 42 A; 104 C; 84 G; 70 T; 0 other;

100.0%; Pred. ...

Conservative

Query Match Best Local Similarity Matches 17; Conserv

2633 ccaggaggcagctcagg 2649

188 ccaggaggcagctcagg 204

cell cycle; mouse; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;

3im-S; Bcl-2 interacting mediator of cell death; apoptosis;

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represent the EST-related proteins corresponding to 242265 to 243052.
The S ESTs can be used for producing secreted human gene products.
They can be used for producing secreted human gene products.
They can be used for producing secreted human gene products.
They can be used for producing secreted human gene products.
They can be used to identify and isolate 5' untranslated regions (UTRS) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide or the insertion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of mew secreted proteins is valuable. Z42249 to be exemplification of the present sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                         Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
Human 5' EST isolated from a cDNA library SEQ ID NO:402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242265 to 243075 represent novel 5' expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 330 BP; 76 A; 102 C; 86 G; 65 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duclert A, Glordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 382; 837pp; English.
                                                                                                                                                           regulation; identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-IB00712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0057719
98US-0069047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-038446/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; Y65029
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                         WO9953051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                      21-0CT-1999
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New isolated member of the Bcl-2 family, Bim used in, e.g. cancer

Claim 3; Page 92; 145pp; English.

treatment

O'Connor L, O'Reilly L;

(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

98WO-AU00772. 97AU-0009373. 97AU-0009263

17-SEP-1998; 24-SEP-1997; 17-SEP-1997;

W09914321-A1

25-MAR-1999

Mus musculus isoform; ss.

Adams J, Cory S, Huang DCS, Puthalakath H, Strasser A;

WPI; 1999-244030/20. P-PSDB; W98154.

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useful in cancer, autoimmune or degenerative disease therapy.
Increased Bim expression or Bim activity is useful, e.g. for
treatment or prophylaxis in conditions such as cancer and deletion
of autoreactive lymphocytes in autoimmune disease. Decreased Bim
expression of Bim activity is useful in regulating inhibition or
prevention of cell death or degeneration such as under cytotoxic
conditions during e.g. gamma-irradiation and chemotherapy or during
HIV/AIDS or other viral infections, ischemia, myocardial infarction,
hypoxia, degenerative diseases or for prolonging the survival of
cells being transplanted for treatment of disease. Since Bim is
expressed in germ cells, modulating Bim expression or Bim activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in therapy, diagnosis, antibody generation and involving modulation of physiological cell death. These therapeutic molecules may act as either antagonists or agonists of Bim's function and will be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; L
1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 17; DB 100.0%; Pred. No. 1.8 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1219 acctcatccaccggac 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 ACCICAICCACCGGAC 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Conservative
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Query Match Best Local Similarity

Matches

The present sequence encodes the short form (5) of murine Bim, or Bc1-2 interacting mediator of cell death (see W98154), a novel comport of the Bc1-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bc1-2 family. Bim is a BH3-only protein, as the conly BH3-only protein for which it encompasses is BH3. It is the only BH3-only protein for which it encompasses is BH3. It is the conly BH3-only protein for which splice variants exist. These result in the expression of a variety of isoforms, i.e. BHm-5, Bim-L and Bim-EL (see W98154-56). cDNAs encoding these murine Bim cerombinant Bc1-2 protein. The murine Bim gene has been mapped to chromosome 2 at bands F3-G. Human Bim-L and Bim-EL isoforms have chromosome 2 at bands F3-G. Human Bim-L and Bim-EL isoforms have chain was shown to regulate the pro-apoptotic activity of Bim. EL. Chain, is a much more potent killer than either Bim-L or Bim-EL. The invention provides variant which does not bind to dynein light chain. Is a much more potent killer than either Bim-L or Bim-EL. That cannot bind, couple or otherwise associate with a dynein light chain. The identification of Bim permits the interpart while distributional design of a range of products for use in the horaw. Alarmosis antiholy departation and rational design of a range of products for use in the horaw.

Gaps ö 0.6%; Score 17; DB 20; Length 332; 00.0%; Pred. No. 1.8e+02; Indels Sequence 332 BP; 87 A; 85 C; 91 G; 69 T; 0 other; Mismatches Query Match 0.6%; Scc Best Local Similarity 100.0%; Pr Matches 17; Conservative 0;

Murine Bcl-2 interacting mediator of cell death Bim-S cDNA.

05-JUL-1999 (first entry)

X24993;

:SSULT 27 %24993/c 72 X24993 standard; cDNA; 332 BP.

is useful, e.g. as a contraceptive or method of sterilization by

preventing generation of fertile sperm.

Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.

Human secreted protein 5' EST SEQ ID NO: 217.

(first entry)

18-JUN-1999

X41005 standard; cDNA; 369 BP

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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNA hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                      Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 347 BP; 61 A; 102 C; 108 G; 75 T; 1 other;
                                                                                  TESULT 28
124629
T T24629 standard; cDNA to mRNA; 347 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1655; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recognising different cell types.
                                                                                                                                                                                                                       Human gene signature HUMGS06689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93JP-0355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-JP01916.
654 aggecteteageagget 670
                                                                                                                                                                                         (first entry)
                Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsubara K,
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              W09514772-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1993;
                                                                                                                                                                                         07-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissues
                                                                                                                                                        T24629;
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New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue

Claim 1; Page 314-315; 622pp; English.

Duclert A, Dumas Milne Edwards J, Lacroix B;

(GEST) GENSET

WPI; 1999-153784/13. P-PSDB; Y12172.

98WO-IB01238 97US-0905134

31-JUL-1998; 01-AUG-1997;

11-FEB-1999.

Homo sapiens. WO9906554-A2

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**X40826 to X41093 represent 5' expressed sequence tags (ESTS) for human secreted proteins, and encode the proteins given in Y01602 and Y11994 to Y12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used for products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, composite activity, composite activity, composite activity, chemotachic/chemokinetic activity, haemastopic activity, haemastopic activity, the activity, composite activity, one other activity, and child mamatory activity, tumour inhibition activity or other activity, and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter for directing extracellular secretion of a polypeptide can be used for directing activity a polypeptide into a membrane, or importing a polypeptide into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 20; 1
Pred. No. 1.8e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X24994/c
ID X24994 standard; cDNA; 422 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 GCCACAGGCCAAGAAGG 304
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Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
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:0; Gaps

0.6%; Score 17; DB 16; Length 347; 100.0%; Pred. No. 1.8e+02; 11ve 0; Mismatches 0; Indels

/ 1336 ccaggaggagtggcag 1352

Best Local Similarity 100. Matches 17; Conservative

Query Match

15 ccaggagggagtggcag 31

ESULT 29

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Bim-L; Bcl-2 interacting mediator of cell death; apoptosis; cell cycle; mouse; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                                   Murine Bcl-2 interacting mediator of cell death Bim-L cDNA.
(first entry)
05-JUL-1999
                                                                                                                                                                                                                                              isoform; ss.
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Mus musculus. W09914321-A1

98WO-AU00772. 97AU-0009373. 97AU-0009263. 24-SEP-1997; 17-SEP-1997; 17-SEP-1998; 25-MAR-1999

O'Connor L, O'Reilly L; (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. Adams J, Cory S, Huang DCS, Puthalakath H, Strasser A;

WPI; 1999-244030/20. P-PSDB; W98155.

New isolated member of the Bcl-2 family, Bim used in, e.g. cancer treatment

Claim 3; Page 94-95; 145pp; English.

The present sequence encodes the long form (L) of murine Bim, or member of the Bol-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the Bol-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bol-2 family. Bim is a BH3-only protein, as the only Bel-2 homology region which splice variants exist. These only Brotesin for which splice variants exist. These only BH3-only protein for which splice variants exist.

Esult in the expression of a variety of isoforms, i.e. Bim-S, Bim-L and Bim-EL (see W98154-56). CDNAS encoding these murine Bim isoforms were obtained from a T lymphoma cDNA library using human chromosome 2 at bands F3-G. Human Bim-L and Bim-EL isoforms have also been identified (see W98157-58). Binding the dynein light chain is a much more potent Killer than either Bim-L or Bim-EL that cannot bind, couple or otherwise associate with a dynein light chain. The identification of Bim permits the with a dynein light chain. The identification of Bim permits the with a dynein light chain. The identification and involving modulation of physiological cell death. These therapeutic molecules may act as either antegonists or agonists of Bim's function and will be useful in cancer, autoimmune or degenerative disease therapy. Increased Bim expression or Bim activity is useful, e.g. for treatment or prophylaxis in conditions such as cancer and delice of prevention of Bim activity is useful, as cancer and delice of prevention of Bim activity is useful, as under cytocxic conditions during e.g. gamma-irradiation and chemotherapy or during e.g. gamma-irradiation and chemotherapy encoditions during e.g. gamma-irradiation and chemotherapy encoditions during e.g. gamma-irradiation and chemotheraph encoditions during e.g. gamma-irrad cells being transplanted for treatment of disease. Since Bim is expressed in germ cells, modulating Bim expression or Bim activity is useful, e.g. as a contraceptive or method of sterilization by

Sequence 422 BP; 112,A; 116 C; 109 G; 85,T; 0 other;

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Gaps

ö

0.6%; Score 17; DB 21; Length 426; 100.0%; Pred. No. 1.8e+02; live 0; Mismatches 0; Indels

32

RESULT

Query Match Best Local Similarity 100.C Matches 17; Conservative

oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes

Sequence 426 BP; 124 A; 81 C; 71 G; 150 T; 0 other;

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Sequences A31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences A32094-A32095 with left and right flanking sequences. The polynuclectide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional choning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for
                                                                                                                                                                                                                                                                                                         Plant microsatellite sequence, core repeat sequence, detection, probe, DNA polymorphism, genome mapping, physical mapping; fingerprinting; variety identification, genetic variability evaluation, primer, ss.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New plant microsatellite markers and associated flanking species {\hbox{\tt for}} the detection of polymorphic genetic markers -
                                 ö
 Length 422;
                               Indels
Score 17; DB 20; L
Pred. No. 1.8e+02;
); Mismatches 0;
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(FLET-) FLETCHER CHALLENGE FORESTS LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Havukkala IJ, Bloksberg LN, Glenn M;
                                                                                                                                                                                                                                                                       Plant microsatellite marker #1030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 379; 392pp; English.
   100.0%; Pre-
                                                                                                                                                                             A32069 standard; DNA; 426 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-NZ00092.
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                                                                 654 aggeeteteageagget 670
                                                                                                                                                                                                                                           (first entry)
                                                                                     75 AGGCCTCTCAGCAGGCT 59
   Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-116958/10.
                                                                                                                                                                                                                                                                                                                                                                          Pinus radiata
                                                                                                                                                                                                                                         05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                        WO9967421-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-DEC-1999.
                                                                                                                                                                                                           A32069;
                                                                                                                                               RESULT 3
A32069/c
                                                                  δ
                                                                                               g
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Location/Qualifiers

Homo sapiens.

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Sequences A31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences A32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design
                                                                                                                                                                                                                                                                                                         Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New plant microsatellite markers and associated flanking species for the detection of polymorphic genetic markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful to locate specific economically useful genes in plant genomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primers for microsatellite-primed PCR. Microsatellite markers are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6%; Score 17; DB 21; Length 431; ).0%; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
(FLET-) FLETCHER CHALLENGE FORESIS LTD.
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Mismatches
                                                                                                                                                                                                                                         Plant microsatellite marker #1013.
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.32052/c
© A32052 standard; DNA; 431 BP.
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                                                                                                                                                                         05-JUL-2000 (first entry)
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Pinus radiata
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                                                                                                   A32052;
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calcium ion channel alpha 1 subunit gene and part of untranslated calcium ion channel alpha 1 subunit gene and part of untranslated sequences. The channel is related to familial hemiplegic migratine (FHM) calcium ion channel is related to familial hemiplegic migratine (FHM) associated with a gene present in humans on chromosome 19p13.1-13.2. The cancoding gene can be used to localise or identify genes related to or encoding gene can be used to localise or identify genes related to or also epilopsy. The isolated or a recombinant nucleic acid can also be used to distinguish between alleles of the corresponding gene. Cells and animals containing recombinant expression vectors comprising the nucleic acid can be useful in study, development and treatment of migraine, FHM.

EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid can be useful in study, development and treatment of migraine, FHM.

EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and natural or synthetic antibodies against the proteins can be used to diagnose FHM. EA-2, migraine and other neurological conditions associated with cation channel disfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences shown in V29330 to V29371 represent the 47 exons and flanking
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human nucleic acid associated with migraine and episodic ataxia type 2 - useful for diagnosis and development of specific treatments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Terwindt GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 17; DB 19; 1
100.0%; Pred. No. 1.8e+02;
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                                                                                          'number= 32
'note= "partial sequence"
                                                                                                                                                                                                                                                                                                                            /note= "partial sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ophoff RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 157pp; English.
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Matches 17; Conservative 0;
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ID X24995 standard; cDNA; 590 BP.
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                                                                                                                                                                                                           'number= 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-195461/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1998
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intron
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δy
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Calcium ion channel alphal subunit exons 33, 34/intron) partial sequence.

V29360 standard; DNA; 559 BP.

TESULT 33

V29360;

31-JUL-1998 (first entry)

Calcium ion channel alphal subunit; human; episodic ataxia type 2; familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis; exon; intron; ss.

Gaps

Length 590;

Score 17; Pred. No.

Sequence 590 BP; 137 A; 178 C; 150 G; 125 T; 0 other;

g

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(HALL-) HALL INST MEDICAL RES WALTER & ELIZA
                                                                                                                                                                                                                                                                                                                                                                                                      Adams J, Cory S, Huang DC:
Puthalakath H, Strasser A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-244030/20.
P-PSDB; W98156.
                                                                  Murine Bcl-2
                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                  W09914321-A1
                                                                                                                                                                                                                                                                                    17-SEP-1998;
                                                                                                                                                                                                                                                                                                                    24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                     17-SEP-1997;
                                 05-JUL-1999
                                                                                                                                                    isoform; ss.
                                                                                                                                                                                                                                                     25-MAR-1999
X24995;
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Bim-EL, Bcl-2 interacting mediator of cell death; apoptosis, cell cycle; mouse; cancer; autoimmune disease; degenerative disease; therapy; contraceptive; splice variant;
                                                       interacting mediator of cell death Bim-EL cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97AU-0009373.
97AU-0009263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-AU00772
(first entry)
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New isolated member of the Bcl-2 family, Bim used in, e.g. cancer treatment

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O'Connor L, O'Reilly

Huang DCS,

Claim 3; Page 96-97; 145pp; English.

The present sequence encodes the extra long form (EL) of murine Bim, or Bol-2 interacting mediator of cell death (see w88156), a novel member of the Bol-2 family that is capable of inducing cell death (apoptosis) and which acts as a 'death-ligand' for certain members of the pro-survival Bol-2 family. Bim is a BH3-only protein, as the only BH3-only protein for which splice variants exist. These only BH3-only protein for which splice variants exist. These result in the expression of a variety of isoforms, i.e. Bim-5, Bim-Land Bim-EL (see w98154-56). CDNAS encoding these murine Bim isoforms were obtained from a T lymphoma cDNA library using human isoforms were obtained from a T lymphoma cDNA library using human isoforms were obtained from a T lymphoma cDNA library using human isoforms were obtained from a T lymphoma cDNA library using human chromosome 2 at bands F3-G. Human Bim-EL and Bim-EL isoforms have also been identified (see w98157-58). Binding the dynein light chain was shown to regulate the pro-apoptotic activity of Bim. Bim-S, the splice variant which does not bind to dynein light chain, is a much more potent Killer than either Bim-I or Bim-EL.

The invention provides variants (see w98159-68) of murine and human Bim-L or Bim-EL that cannot bind, couple or otherwise associate with a dynein light chain. The indentification of Bim permits the intentional design of a range of products for use in therapy, diagnosis, antibody generation and involving modulation of physiological casi death. These therapeutic molecules may act as either antagonists or agonists of Bim's function and will be useful in cancer, autoimmune or degenerative disease therapy. Increased Bim expression or Bim activity is useful, e.g. for treatment or prophylaxis in conditions such as cancer and deletion of autoreactive lymphocytes in autoimmune disease. Decreased Bim expression of Bim activity is useful in regulating inhibition or prowention of cell death or degeneration such as under cytotoxic conditions during e.g. amma-irradiation and chemotherapy or during HIV/AIDS or other viral infections, ischemia myocardial infarction, cells being transplanted for treatment of disease. Since Bim is expressed in germ cells, modulating Bim expression or Bim activity hypoxia, degenerative diseases or for prolonging the survival of cells being transplanted for treatment of disease. Since Bim is is useful, e.g. as a contraceptive or method of sterilization by preventing generation of fertile sperm.

31 gttttggtggagacggg 47

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This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, chemotactic/chemokinetic activity, activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
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                                                                                                                                                                                                                                                                                                       tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding human secreted proteins - derived from
                                                                                                                                                                                                                                                                                          secreted protein; haematopoiesis regulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. human blood, kidney, foetal lung, placenta, testes, brain. ovary, pituitary, retina and colon cDNA libraries
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                                      Indels
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       DB 20; L
1.8e+02;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 20; I
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lavallie ER,
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 486; 633pp; English.
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100.0%; Pre
0; 7
0.6%; St.
100.0%; Pre
                                                                                                                                                                      V87198 standard; cDNA; 605 BP.
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                                                                  654 aggeoteteageagget 670
                                                                                                                                                                                                                               27-APR-1999 (first entry)
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                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                          Expressed sequence tag;
                                                                                              75 AGGCCTCTCAGCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-070076/06.
         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Lora
                                                                                                                                                                                                                                                              EST clone BN180.
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                WO9845435-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agostino MJ,
Racie LA, S<sub>l</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy.
                                                                                                                                                                                                    V87198;
                                                                                                                                           35
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                                                                                                                                         RESULT 3
V87198/c
ID V871
XX
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severity of an immune response or to treat cancer. TRAIN-R blocking agents can also be used to reduce the severity or effects of an immunological disease (all claimed).

Sequence 791 BP; 202 A; 189 C; 165 G; 235 T; 0 other;

Ouery Match

0.6%; Score 17; DB 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0;

2130 gaagaggaagcagtgga 2146

ŏ g

203 GAAGAGGAAGCAGTGGA 187

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Gaps

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Length 791; Indels

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The present sequence includes an exon encoding the C-terminus (see W98147) of a soluble form of a novel human cysteine-rich tumour necrosis factor receptor family member termed TRAIN-R. It comprises clone GJ156, obtained from a Clontech human adult lung cDNA ilbrary. The encoded 30-amino acid C-terminal peptide is identical to amino acids 121-149 of the composite TRAIN-R protein given in W98146 and to amino acids 121-150 of the C-terminus of murine TRAIN-R short form (secreted protein, see W98144). The soluble protein is expected to inhibit signalling by the full-length TRAIN-R. Human TRAIN-R is expressed at low levels in every tissue and cell line tested thus far, with higher expression detected in heart, prostate, ovary, testis, peripheral blood lymphocytes, thyroid and adrenal gland. Cell death can be induced by administering an agent capable of inhibiting the binding of TRAIN-R to its ligand. A claimed method of treating, or reducing, the advancement, severity or effects of an immunological disease in a mammal comprises administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "TRAIN-R secreted form C-terminus" 45..790
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                               TRAIN-R; receptor; human; tumour necrosis factor receptor; agonist; antagonist; cancer; immunological disease; therapy;
                                                                                                                                                                                                                                                                                                                                                          Clone GJ156 encoding TRAIN-R secreted form C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cysteine-rich tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1..350
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                                                                                                                                                                             ВР
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                                                                                                                                                                             X24979 standard; cDNA; 791
212 GTTTGGTGGAGACGGG 196
                                                                                                                                                                                                                                                                                               (first entry)
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351..790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-229238/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W98147
                                                                                                                                                                                                                                                                                                                                                                                                                                                 agonist; antag
cytostatic; ss
                                                                                                                                                                                                                                                                                               05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9913078-A1.
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                                                                                                                                                                                                                                        X24979;
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74979/
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This sequence encodes a Streptococcus pneumoniae protein of the invention. The proteins (or their homologues, derivatives and/or fragments) are useful as immunosopens or antigens. Immunosopenic or antigenic compositions comprising the proteins are useful as vaccines and also in diagnostic assays. The sequences are useful for the detection or diagnostic assays. The sequences are useful for the detection or compositions is of a preumonate infection, by contacting a sample to be tested with them. Agents, capable of antagonising, inhibiting or interfering with the function or expression of the protein or prophylaxis of S. pneumoniae infection. As the sequences can be used to treat S. pneumoniae infection, they can be used to treat bacterial pneumonia, which has high rates in young children, the elderly, and in patients with predisposing conditions such as asplenia, heart, lung and kidney disease, diabetes, alcoholism, or with immunosuppressive disorders, especially AIDS. They can also be used to treat pneumococcal septicaemia, otitis media, sinusitis, and
                                                                                                                                                                                  Streptococcus pneumoniae infection; immunogen; antigen; diagnosis; AIDS; bacterial pneumonia; asplenia; heart disease; lung disease; alcoholism; kidney disease; diabetes; immunosuppressive disorder; otitis media; pneumococcal septicaemia; sinusitis; meningitis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcal proteins and polynucleotides useful for diagnosis, treatment and prophylaxis of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hansbro PM;
                                                                                                                                                  Streptococcus pneumoniae DNA sequence ID33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Le Page RWF, Wells JM, Hanniffy SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 47-48; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROBIAL TECHNICS LTD
                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       98GB-0016336.
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-GB02452
                                                                                                            (first entry)
                                     291823 standard; DNA; 855
                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                        WO200006738-A2
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                                                                                                            02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1999;
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19-MAR-1999;
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                                                                           291823;
RESULT 37
                   Z91823
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Sequence 855 BP; 235 A; 173 C; 202 G; 245 T; 0 other;

pharmaceutical composition which comprises a TRAIN'R blocking agent, e.g. soluble TRAIN'R. TRAIN'R can be fused to an immunoglobulin to produce a fusion protein which may be targeted to various sites. It can be used in binding assays, and to identify antagonists and agonists. Anti-TRAIN'R antibodies can be used to reduce the

X40199;

38

RESULT X40199

1947

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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                      RESULT
Q67866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers \frac{1}{2}
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                   Length 855;
                 0.6%; Score 17; DB 21; Length 85
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                old LJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'Hare M, Obata Y, Old
Scanlan MJ, Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1022 BP; 230 A; 273 C; 302 G; 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                     X40199 standard; DNA; 1022 BP
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97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
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                                                                                                     Gure A,
Sahin U,
                                                                                                                                               139 gatttggaagagtttca 155
                                                                                                                                                                                                                                                                                                                                          (first entry)
                   Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 MAGE-4 encoding gene.
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P-PSDB; Y06998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfreundschuh M,
Tureci O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9904265-A2
                                                                                                                                                                                                                                                                                                                                          02-JUL-1999
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10-OCT-1997
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Length 1022;

Score 17; DB 20;

0.68;

Query Match

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                                                                                                                                                                                                                                                                                                                                 Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; MAGE-1; melanoma-associated antigen; MZ-E; testis; pTZ18RMAGE1; primary melanoma tumour cell; melanoma derived cell line; tumour; poxvirus; antigenic response; immunological response; pathogen; ss.
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprises
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0
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Attenuated recombinant virus used for cancer therapy - DNA encoding cytokine and/or tumour associated antigen
              Pred. No. 1.7e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "Vaccinia H6 promoter"
                                                                                                                                                                                                                                                                                                 H6/MAGE-1 expression cassette from pMAW037.
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/note= "Flanking sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
"Flanking sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product MAGE-1
100.08; PI
                                                                                                                                                                                          Q67866 standard; DNA; 1084 BP.
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94US-0184009.
                                                                  1652 ggtcctgggcaccctgg 1668
                                                                                                     203 ggtcctgggcacctgg 219
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                                                                                                                                                                                                                                                                22-MAR-1995 (first entry)
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                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-263767/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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19-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
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ALVAC and NYVAC. The resulting viruses may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation against pathogens.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H6/MAGE-1 expression cassette and flanking regions from pMAW037.
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                                                                                                                                                                                             Query Match 0.6%; Score 17; DB 15; Length 1084; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 17; Conservative 0; Mismatches 0; Indels (
                                                                                                               Sequence 1084 BP; 266 A; 256 C; 280 G; 282 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z08442 standard; DNA; 1084 BP.
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820S-0446824.
840S-0622135.
870S-0090209.
870S-0090711.
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90US-0537882.
90US-0537890.
91US-0638080.
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89US-0320471
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94US-0306259
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91US-0713967
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92US-0847977
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292 ggtcctgggcaccctgg 308
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Vaccinia virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-OCT-1999
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25-APR-1988
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27-AUG-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      .SSULT 40
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The interpolation of the recombination of the recombination of the refore induces an immunological response. (I) may be used to vaccinate patients against a wide range of diseases and disorders be used to vaccinate against a wide range of diseases and disorders be used to vaccinate against diseases such as rabbies, influenza and Newcastle Disease. It is particularly useful for immunising against lymphocytes and tumour cells for use in cell-based immunotherapeutic modalities for cancer. (I) also have enhanced safety compared to unattenuated viruses (attenuation reduces the virulence of the viruses) and known recombinant poxvirus vaccines. This increased level of safety reduces the possibility of a 'tunaway' infection in the host and reduces the chance of transmission from vaccinated to unvaccinated individuals
                                                                                                                                                                                                                                                                                                                                                                                                           and contamination of the environment. The present sequence represents a H6/MAGE-1 expression cassette and flanking regions from pMAW037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; MAGE-1; melanoma-associated antigen; MZ2-E; testis; pTZ18RWAGE1; primary melanoma tumour cell; melanoma-derived cell line; tumour; poxvirus; antigenic response; immunological response; pathogen; ss.
                                                                                                                                         The present invention describes a recombinant poxvirus (I), comprising exogenous DNA encoding an antigenic determinant of a pathogen which is then expressed in vivo in infected host cells after administration to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                               Recombinant poxviruses comprising exogenous DNA encoding antigenic determinants useful in immunotherapy to immunize against cancers and other diseases such as influenza, Newcastle Disease and rabies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1084 BP; 266 A; 256 C; 280 G; 282 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 17; DB 20; I
.00.0%; Pred. No. 1.7e+02;
.ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "Vaccinia H6 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H6/MAGE-1 expression cassette from vCP235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/note= "Flanking sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
74..200
                                                                                                       Example 16; Fig 20; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/product= MAGE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q67865 standard; DNA; 1094 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
WPI; 1999-493494/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9416716-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    067865;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 41
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23

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Recombinant poxviruses comprising exogenous DNA encoding antige determinants useful in immunotherapy to immunize against cancer other diseases such as influenza, Newcastle Disease and rabies
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                                                             88US-0186054.
88US-0234390.
89US-0320471.
90US-0478179.
                                                                                                                                                                                                                                                                                 94US-0228926
94US-0306259
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                                       870S-0090
870S-0110
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                                                                                                                    00S-053
                                                                                                                                                                                                                                                                                                                            RES INC
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-493494/41.
                                                                                                                                                                                                                                                                                                                           (HEAL-) HEALTH
                                                                                                                                                                                                                                                                                                  13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                      Paoletti E;
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                                                                                3-AUG-1
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                                                                                                           FEB-
  δλ
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                                                                                                                                                                                               containing the vaccinia He promoter and the human MAGE-1 gene which encodes human melanoma-associated antigen MZ2-E, in vCP235 and pMAW037, respectively. These sequences were used in the construction of NYVAC- and ALVAC-based recombinant viruses containing the MAGE-1 gene. MAGE-1 is expressed in primary melanoma tumour cells, melanoma-derived cell lines and certian tumours of non-melanoma origins but not in normal cells except in testis. A first profit fragment containing the last 18 bp and the initial 24 nucleotides of the MAGE-1 gene was generated and igated to a second PCK fragment amplified from plasmid pT218RAMGE1 which contains the initial 546 bp of the MAGE-1 coding sequence. The terminal sequence of MAGE-1 was amplified and a fusion product was generated containing the H6 promoter and the full length MAGE-1 sequence. This construct may be introduced in to the poxylius derived plasmids. ALVAC and NYVAC. The resulting viruses may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Attenuated recombinant virus; cytokine; tumour associated antigen; NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rables; cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF; interleukin; interferon; IFN-gamma; IL-4, melanoma associated antigen; carcinoembryonic antigen; immunoisation; antigenic; poxvirus; influenza; immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps

    comprises

                                                                                                                                                                                        The sequences given in 067865-66 represent expression cassettes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H6/MAGE-1 expression cassette and flanking regions from vCP235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                    Attenuated recombinant virus used for cancer therapy - DNA encoding cytokine and/or tumour associated antigen \,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1094 BP; 269 A; 259 C; 293 G; 273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 15; L
Pred. No. 1.7e+02;
0; Mismatches 0;
                                                                                                                                                             Example 16; Fig 19; 232pp; English
                                                                   Tartaglia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Scc.
100.0%; Pre
0; }
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81US-0334456
93US-0007115.
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Best Local Similarity 100.0
Matches 17; Conservative
                                        (VIRO-) VIROGENETICS CORP
                                                                   ы
                                                                                           WPI; 1994-263767/32
                                                                                                                                                                                                                                                                                                                                                                                                             against pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Vaccinia virus.
21-JAN-1993;
19-JAN-1994;
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24-DEC-1981;
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                                                                  Cox WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 42
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ogenous DNA encoding antigenic to immunize against cancers and

1US-0805567 2US-0847977

1US-0713967

3US-0007115

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                                                                                               patient and therefore induces an immunological response. (I) may be used to vaccinate patients against a wide range of diseases and disorders depending on the type of antigen encoded by the exogenous DNA. (I) may be used to vaccinate against diseases such as rables, influenza and Newcastle Disease. It is particularly useful for immunising against cancers. The poxyrius (I) also provides a means of manipulating modalities for cancer. (I) also have enhanced safety compared to mattenuated viruses (attenuation reduces the virulence of the viruses) and known recombinant poxyrius vaccines. This increased level of safety reduces the possibility of a 'runaway' infection in the host and reduces
The present invention describes a recombinant poxvirus (I), comprising exogenous DNA encoding an antigenic determinant of a pathogen which is then expressed in vivo in infected host cells after administration to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                          and known recommence.

reduces the possibility of a 'runaway' infection in the possibility of a 'runaway' infection of transmission from vaccinated to unvaccinated individuals the chance of transmission from vaccinated to unvaccinated individuals and contamination of the environment. The present sequence represents and contamination of the environment. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1094 BP; 269 A; 259 C; 293 G; 273 T; 0 other;
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ID X27353 standard; DNA; 1140 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 ggtcctgggcacctgg 330
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11-JUN-1999 (first entry)
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Human secreted protein gene 43 clone HTADX17

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obseity; osteoclast; thymus, osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens

WO9902546-A1

21-JAN-1999.

98WO-US13684 07-JUL-1998; 970S-0058785. 970S-0051916. 970S-0051918. 970S-0051919. 970S-0051920.

97US-0051925. 97US-0051926. 97US-0051928. 97US-0051929 97us-0051930 97US-0051931

97US-0052732 97US-0051932 97US-0052793 97us-0052795

97us-0052803 97US-0055723 97US-0055 97US-00 .8-AUG-1997 8-AUG-1 8-AUG-

97US-0055948 97US-0055949 97us-0055950 97US-0055954 97US-0055953 18-AUG-1997 .8-AUG-1997 18-AUG-1997 8-AUG-1997 18-AUG-1997

97US-0058664 97US-0058660 97US-0055984 12-SEP-1997 18-AUG-1997 L2-SEP-1997

97US-0055964

18-AUG-1997

(HUMA-) HUMAN GENOME SCI INC

Y, Moore PA; DW, Li Zeng Z; Fischer CL, Kyaw H, Lafleur Ruben SM, Shi Y, Soppet DR, Ebner R, Rosen CA, Brewer LA, Olsen HS,

WPI; 1999-120770/10. P-PSDB; Y02692.

New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 271; 464pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. x27302) for increasing the stability of the fused protein as

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Gaps

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Indels

1.7e+02;

Pred. No. 1.7 Mismatches

294 cggtatctcttcaactg 310

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compared to the human protein only.

The invention relates to 123 novel genes and their fragments (nucleic acid sequences: X27311-X27449; amino acid sequences Y02650-Y02788) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 123 polynucleotides, based on which tissues they are most highly expressed in (see X27311 for described
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening; PCR; primer; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the 3' region of hepatitis C virus RNA. The original sample was obtained from human and chimpanzee plasma. RNA was isolated from several samples and homology compared, and the respective sequence of about 1900 - 2500 nucleotides of the 5'
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide primers with nucleotide sequences corresp. part. of the viral RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1173;
                                                                                                                                                                                                                                         Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       terminus and 1100 nucleotides of the 3' terminus determined
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                        Sequence 1140 BP; 280 A; 312 C; 289 G; 254 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1173 BP; 246 A; 358 C; 310 G; 259 T; 0 other;
                                                                                                                                                                                                                                      0.6%; Score 17; DB 20; L 100.0%; Pred. No. 1.7e+02; ... ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 17; DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 28; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus HC-J5 3' region.
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                          Q29634 standard; DNA; 1173 BP
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                                                                                                                                                                                                                                                                                                                                          930 caaagcctggctccagc 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                         Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMO ) IMMUNO JAPAN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura I, Okamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP510952-A.
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                                                                                                                                                          uses).
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Hepatitis C virus

16-MAR-1993

029635 029635;

TESULT 129635

Ω,

23-APR-1992; 26-APR-1991;

28-OCT-1992 EP510952-A.

Nakamura T,

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Forkhead activin signal transducer protein; FAST2; activin signalling; winged-helix/forkhead domain protein; homeobox gene; goosecoid inducer; gsc; transforming growth factor-beta signalling; gsc promoter; signal transduction; transcription factor; wound healing; inflammation; tumour progression; scarring; arthritis; fibrosis; liver fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "Forkhead activin signal transducer protein"
//transl_except= (pos: 1183..1185, aa: Cys)
                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of NANB hepatitis virus polynucleotide N-1173-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding a forkhead activin signal transducer designated FAST2.
                                                                                                                                                                                                                                                                                                                                                                                                        which codes for a non-A, non-B (NANB) hepatitis virus gene HC-OM. The polypeptide it encodes may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by
                                                                                                                                                                                                                                                                              non-translation region comprising 340 - 341 mols. of nucleotides, nucleotides including region 1,149 and, etc.
                                                                                                                                                                                                                                                                     Antigen related to non-A and non-B hepatitis virus - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 1173;
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1173 BP; 247 A; 358 C; 309 G; 259 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 29; 73pp; Japanese.
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100.08;
0;
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90JP-0304405
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Best Local Similarity 100.
Matches 17; Conservative
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conventional methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrosis; ss.
                                                                                                                                                                                                                    WPI; 1993-199637/25
                                                                                                                                                                                     (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                      P-PSDB; R38285
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                                 JP05091884-A
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                                                                                                  10-APR-1991;
                                                                                                                                  12-JUN-1990;
08-NOV-1990;
                                                                  16-APR-1993.
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246089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the 3' region of hepatitis C virus RNA. The original sample was obtained from human and chimpanzee plasma. RNA was isolated from several samples and homology compared, and the respective sequence of about 1900 - 2500 nucleotides of the 5' terminus and 1100 nucleotides of the 3' terminus determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                  Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide primers with nucleotide sequences corresp. part. of the viral RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-A, non-B; virus; polymerase chain reaction; detection; sensitive; specific; HCV; NANBH; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1173 BP; 251 A; 362 C; 304 G; 256 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; I
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NANB hepatitis virus polynucleotide N-1173-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 1
Pred. No. 1.76
0; Mismatches
                                                                                                                                                                                                                                    PCR; primer; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q43895 standard; cDNA to RNA; 1173 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 29; 54pp; English
                                                                                                                                                                                   Hepatitis C virus HC-J6 3' region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.6%; So
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-B hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                      92EP-0303625
                                                                                                                                                                                                                                                                                                                                                                                                        91JP-0191376
                                                                                  standard; DNA; 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 cggtatctctcaactg 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
910 eggtatetetteaactg 926
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMO ) IMMUNO JAPAN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamoto H;
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21-0CT-1993

Non-A, Key

043895;

TESULT 46 043895 1D 043895 XX

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Gaps

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WO9940188-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                X87591;
                                                                    breast
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                X87591
                                                                                                                                                                                                                                                                                                                                                              οy
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                                                                                                                                                                      The present sequence encodes a mammalian forkhead activin signal transducer (FAST) protein, designated FAST2. The protein is a winged-helix/forkhead domain protein. The protein is an inducer of the homeobox gene goosecoid (gsc) by transforming growth factor (TGF)-beta or activin signaling. FAST2 binds to a nucleotide sequence in the gsc promoter. The FAST2 protein is useful for modulating signal transduction in a TGF-beta or activin signaling pathway, which involves FAST2 as transcription factor, by modulating the formation of FAST2 Smad2/Smad4/FAST2 complex. Inhibition of FAST2
                                                                                                                                                                                                                                                                         binding to its target DNA site inhibits FAST2 specific TGF-beta signaling, which is associated with wound healing inflammation, and tumour progression. Excessive signaling is associated with scarring, arthritis and fibrosis in numerous diseases, including fibrosis of the liver and kidney.
                                                                                                 New mammalian transcription factor, useful for preventing or treating disorders associated with transforming growth factor beta or activin signaling pathways ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast cancer; bladder cancer; lung cancer; colon cancer; head and squamous cell carcinoma; oesophagus carcinoma; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 21; Length 1209;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAGE-1; CLYTA-MAGE-1-His; fusion protein; tumour; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 1209 BP; 247 A; 412 C; 315 G; 235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.6%; Score 17; Db
Best Local Similarity 100.0%; Pred. No. 1.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Streptococcus pneumoniae.
Chimeric - Homo sapiens.
Chimeric - synthetic.
                                                                                                                                                   Claim 3; Page 43; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X87593 standard; cDNA; 1338 BP
98CA-2237788
                                                                                                                                                                                                                                                                                                                                                                                                                               1074 cacatggccccagcatc 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLYTA-MAGE-1-His fusion DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-EP00660
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98GB-0002543
                                                                                                                                                                                                                                                                                                                                                                                                                                                      636 cacatggccccagcatc 652
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                      (HSCR-) HSC RES & DEV LP
                                            Wrana JL, Attisano L;
                                                                    WPI; 2000-171267/15
                                                                               P-PSDB; Y54601.
17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9940188-A2
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05-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 48
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protein (CIVTA), the human MAGE-1 tumour-associated antiqen and hexahistidine tail. A vector designed for recombinant expression of the fusion protein in Escherichia coli is provided. The CIVTA moiety provides expression of soluble fusion protein, facilitates affinity purification of the fusion protein, and also acts as a finity purification of the fusion protein, and also acts as a finity purification of the fusion protein, and also acts as a mimunological fusion partner, e.g. Clyta-MAGE-1-His. These novel fusion proteins provide vaccines for immunotherapy of melanomas or other MAGE-associated tumours like breast, bladder, lung and non-small cell lung cancer, head and squamous cell carcinoma, colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                      New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of
                                                                                                                                                                                                                                                                                                                      This DNA sequence codes for a fusion protein (see Y06592) composed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGE-1; lipoprotein D; LPD-MAGE-1-His; fusion protein; tumour; melanoma; breast cancer; bladder cancer; lung cancer; head and squamous cell carcinoma; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1338 BP; 335 A; 334 C; 378 G; 291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%; Score 17; DB 20; I
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 1... tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oesophagus carcinoma; vaccine; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                Example 9; Page 70-71; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein D-MAGE-1-His fusion DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carcinoma and oesophagus carcinoma.
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Chimeric - Homo sapiens.
Chimeric - synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X87591 standard; cDNA; 1341 BP.
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98GB-0002543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.69
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 ggtcctgggcacctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-494293/41.
P-PSDB; Y06590.
WPI; 1999-494293/41.
P-PSDB; Y06592.
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See also 013729-013733.

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Gaps
                                                                                                                            invention relates to MAGE proteins fused to an immunological fusion partner such as LPD. The LPD molety provides the fusion protein with additional exogenous T-cell epitopes and also increase expression levels in E. coli. The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. The affinity tag facilitates purification. The novel fusion proteins provide vaccines for immunotherapy of melanomas or other MAGE-associated tumours like breast, bladder, lung and non-small and oesophagus carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is shown folded into secondary structure in the specification. It was compared with other sequences available in the literature to design probes specific for SRB. The probes can be used for the rapid identification and quantification of SRB in a sample, e.g. oil-field prodm. waters, water from water treatment facilities, or samples from the gut of ruminant animals.
                                                                                  of Haemophilus influenzae B, the human
                                          Is DNA sequence codes for a fusion protein (see Y05590) composed lipidated protein D (LPD) of Haemophilus influenzae B. the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assay for sulphate-reducing bacteria - by hybridisation using a labelled oligo-nucleotide probe corresponding to 16S rRNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1341;
                                                                                                           MAGE-1 tumour-associated antigen and a hexahistidine tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRB; Desulphovibro; Desulphotomaculum; ribosomal RNA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1341 BP; 336 A; 327 C; 351 G; 327 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16S RNA from ATCC 19858 sulphate-reducing bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
Example 6; Page 66; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14450/c
'2 Q14450 standard; RNA; 1345 BP.
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1652 ggtcctgggcacctgg 1668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-0339277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STAH ) STANDARD OIL CO. (OHIO ) OHIO OIL CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brink DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-294983/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                        This DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes a protein which can release G1 arrest of an animal cell. This sequence was isolated from a human foreskin cDNA library. The protein can be used in the control of the cell
                                                                                                                                                                                                                                                                 cDNA encoding protein for releasing G1 arrest in an animal cell.
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Pred. No. 1.7e+02;
                                                      Length 1345;
                                                                                Indels
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/note= "Given in the specification as 5"
                  Sequence 1345 BP; 331 A; 297 C; 435 G; 249 U; 33 other;
                                                                                                                                                                                                                                                                                       Gl arrest; animal cell; human foreskin; cell cycle; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1557 BP; 438 A; 349 C; 363 G; 406 T; 1.other;
                                                       DB 12; L
1.7e+02;
thes 0;
                                                       Score 17; DB ]
Pred. No. 1.76
0; Mismatches
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280..1290
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                                               0.6%; SCUL
100.0%; Pre
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T27644 standard; cDNA; 1557 BP.
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198595 standard; DNA; 1591 BP
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                                                                                                                               1274 CGGCTTTCTCAGTTTTG 1258
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                                                                                Conservative
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P-PSDB; R96248.
                                                                  Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         JP08092288-A
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                                                          Query Match
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T98595/c
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Streptococcus

WO9743303-A1

CDS

20-NOV-1997

14-MAY-1997; 14-MAY-1996;

Black MT, 1 Stodola RK;

infections

DNA encoding 06-NOV-1998

T98595;

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conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of a Streptococcal polypeptide coding region. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media,
                                                                                                                                                                                                                                                                                        Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 1592 BP; 454 A; 317 C; 376 G; 445 T; 0 other;
                                                                                                                                                                                                                                              Streptococcus pneumoniae polypeptide coding region.
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Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 56-57; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 573..1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Scc.
100.0%; Pre
0; }
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                                                                                                            V42963 standard; DNA; 1592 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1158 gatttggaagagtttca 1174
435 GATTTGGAAGAGTTTCA 419
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zarfos PN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reid RH,
                                                                                                                                                        V42963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V68059;
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V68059
                                                                   RESULT
V42963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-bonology with Streptocicus minding proteins) are GTP-binding proteins ERR homolog, and represents a DNA sequence of the invention. The DNA sequence of the invention. The DNA sequences were isolated from Streptococcus pneumoniae strain oloo993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the invention can be used to identify compounds which interact with and inhibit or activate the activity of the proteins. Antagonists can be used to incertain and interact with and inmunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antithody andor T cell immune responses to protect the animal from disease. The proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein-mediated mammalian cell invasion, and to block the normal progression of pathogenesis in infections initiated other than by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                           immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound; pathogenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial
                                                                                                                                                        pneumoniae protein; genetic immunisation; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence encodes two Streptococcus pneumoniae proteins (based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in-dwelling devices or other surgical techniques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1591 BP; 452 A; 378 C; 313 G; 448 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knowles DJC, Nicholas RO;
                                                                                                            GTP-binding proteins ERA homolog.
                                                                                                                                                                                                                                                                                                                                                                                                  complement (1022..1492)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Pages 129-130; 483pp; English.
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers complement (592..1086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
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                                                                   (first entry)
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                                                                                                                                                                                                                                                                                          pneumoniae.
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P-PSDB; W38537, W38538.
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Nicholas RO;

Lonetto MA,

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Gaps

; 0

Indels

implantation of

Length 1592;

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(MILL-) MILLENNIUM PHARM INC. (CRCT-) CRC TECHNOLOGY LTD.
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Matches 17; Conservative
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                                                                                             WPI; 1999-562123/47
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                                                               Graham GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V72116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 56
V72116
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                             Neurodegenerative polypeptide; HHPDZ65; stroke; pain; epilepsy; therapy; neurodegenerative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide of the invention. HHPDZ65 is useful for the treatment of stroke, pain, epilepsy, neurodegenerative diseases and others. The DNAs and proteins are useful in a method for screening to identify compounds which stimulate or inhibit the function of the HHPDZ65 proteins. The polypeptides are useful in a process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the HHPDZ65 polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                  HHPDZ65 polypeptide(s), their corresponding DNA, antibodies, agonists and antagonists - are useful in the treatment of stroke, pain, epilepsy and neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1632;
Neurodegenerative polypeptide HHPDZ65var coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the HHPDZ65var neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1632 BP; 312 A; 529 C; 497 G; 294 T; 0 other;
                                                                                                                                                                                                                                                                                                       Topp S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%; Score 17; DB 19; 300.0%; Pred. No. 1.7e+02; ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      Harrison DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine D6 encoding cDNA SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.0%,
100.0%; Pie
                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Page 16; 31pp; English.
                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                      Doe TR,
                                                                                                                                                                                                       98GB-0003566.
97GB-0008936.
97EP-0310289.
                                                                                                                                                                       98EP-0302912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1579 cacggtccccaggagg 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z25023 standard; cDNA; 1664
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                                                                                                                                                                                                                                                                                                      Davis J,
                                                                                                                                                                                                                                                                                                                                    WPI; 1998-559436/48.
P-PSDB; W80318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09947697-A1
                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1998;
                                                                                                                                                                       15-APR-1998;
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                                                                                                          EP875570-A2
                                                                                                                                                                                                                        01-MAY-1997
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                                                                                                                                        04-NOV-1998
                                                                                                                                                                                                                                      18-DEC-1997
                                                                                                                                                                                                                                                                                                      Bingham S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
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Methods have been developed for identifying a compound, which binds to a human or murine D6 protein, an allelic variant or a fragment comprises detecting binding of the test compound to the protein. Also described in the present invention are: (1) a method for identifying a compound capable of treating a disorder characterised by aberrant D6 nucleic acid expression of D6 protein activity; (2) a method for treating a subject having a disorder characterized by aberrant D6 nucleic acid expression comprising administering to the subject a D6 modulator such that treatment of the subject occurs; and (3) methods for identifying a compound that modulates the activity of a Human or murine D6 protein, an allelic variant or a fragment. The methods are useful for identifying compounds capable of treating disorders, especially a respiratory inflammatory disorder, characterized by aberrant D6 nucleic acid expression or D6 protein activity. In particular, the disorder is asthma. D6 modulators are used to treat asthma. The present sequence encodes the murine D6 protein.
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                                                                                                                                                                                       Identification of D6 G-protein coupled receptor binding compounds and modulators, useful in treatment of asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1664;
       Gutierrez-Ramos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 20; I
Pred. No. 1.7e+02;
); Mismatches 0;
   Gonzalo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08; Fr.
Benjamin Nibbs RJ,
                                                                                                                                                                                                                                                                                                          Claim 2; Fig 2; 152pp; English.
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Thu Feb 22 15:01:06 2001

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a method to detect a compound capable of modulating transforming growth factor-beta (TGT-beta) superfamily signalling. The invention describes accomplex which forms between FAST-1 and Smad2 and this complex is specifically induced by signals generated by a TGF-beta superfamily member. A domain of FAST-1 directly interacts with Smad2 and this molecules, namely, the MH2 domains of the two interacting molecules, namely, the MH2 domain of Smad2 and the Smad interacting for the detection and treatment of conditions involving abnormal TGF-beta superfamily signalling. They can be used to treat e.g. developmental disorders, immunological disorders and cancer. The products can also be
                                                        Modulating TGF-beta superfamily signalling - comprises use of compounds identified in assays with Smad2, FAST-1 and Smad3, used develop products for treating, e.g. developmental disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes a mouse FAST-1 protein which is used in
                                                                                                                                                                                                                                                                                                                                                                                     Example XII; Page 70; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used for detection and diagnosis.
SECTION SUPPLIES SECTION SECTI
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Sequence 1668 BP; 368 A; 517 C; 432 G; 351 T; 0 other;

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Gaps
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       Score 17; DB 20; Length 1668; Pred. No. 1.7e+02; 0; Mismatches 0; Indels
0.6%; Scor.
100.0%; Pred. No. 1...
... 0; Mismatches
                                                                     1074 cacatggccccagcatc 1090
                       Best Local Similarity 100.
Matches 17; Conservative
           Query Match
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621 cacatggccccagcatc 637

57

V69719 standard; cDNA; 1691 BP V69719;

01-MAR-1999 (first entry)

Tumour rejection antigen precursor MAGE-Al cDNA.

ONDRESSENT NAME ON THE

tumour rejection antigen precursor; TRAP; MAGE-Al; human; tumour therapy; diagnosis; ss.

Homo sapiens

Location/Qualifiers 204 .1133 /*tmg= a

WO9849184-A1. 05-NOV-1998 98WO-US08493. 24-APR-1998; 97US-0845528 25-APR-1997; (LUDW-) LUDWIG INST CANCER RES

De Smet C, Boon-Falleur T,

WPI; 1999-024041/02. P-PSDB; W81548.

RECEIVE

Tumour rejection antigen precursors – used for determining presence of cytolytic T cells specific for complexes of a human leukocyte antigen

Disclosure; Page 46-47; 84pp; English.

Sequence 1702 BP; 371 A; 517 C; 476 G; 338 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. $25888-$23014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in $73814-$774252.
This nucleotide sequence comprises human tumour rejection antigen precursor (TRAP) MAGE-Al cDNA, which encodes a 309-amino acid college by 1901 peptide (see W8154B). MAGE-Al cDNA shows homology to novel human MAGE-Cl cDNA (see V65720), especially in exons 2 and 3.

The open reading frame of MACE-Cl, however, is about 2 kb longer than that of MAGE-Al most of the difference being accounted for by a large repetitive sequence. MAGE-Cl (see W81546) is a novel member of the MAGE family that may be recognised by cytotoxic rells, leading to lysis of the tumour cells which express it. It is expressed in a variety of tumours and in normal testis cells, but not by other normal cells. The invention provides MACE-Cl and MACE-C2 nucleic acids and polypeptides, useful e.g. in a claimed method for determining the presence of cytolytic I cells specific
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human nucleic acid sequences from pancreatic tumors, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor; EST; expressed sequence tag; human; cytostatic;
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                                                                                                                                                                                                                                                                                                            Length 1691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate tumor cDNA library derived EST fragment #19
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                          Sequence 1691 BP; 410 A; 389 C; 465 G; 427 T; 0 other;
                                                                                                                                                                                                                              for complexes of a human leukocyte antigen (HLA).
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                                                                                                                                                                                                                                                                                                              Score 17; DB 20; 1
Pred. No. 1.7e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                 0.6%; Scor.
100.0%; Pre
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P-PSDB; Y73868, Y73869, Y73870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252876 standard; cDNA; 1702
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pancreas;
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1565 agggagtggcagaggga 1581

X85940 standard; DNA; 1816

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RESULT

x85940

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                                                                                                                                                                                                                                                                                                                                                                                                                              Beta(1 -> 4)-N-acetylglucosaminyl-transferase; GnT-IV; bovine; human;
enzyme; sugar chain subunit; branched oligosaccharide; polysaccharide;
drug; reagent; food; blopolymer; glycoprotein; erythropoletin; ss.
                                                                                                                                                                                                                                                                                                                                                                                       Beta(1 -> 4)-N-acetylglucosaminyl-transferase (GnT-IV)b encoding cDNA.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
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                Length 1702;
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                                                         0; Indels
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         Score 17; DB 20;
Pred. No. 1.7e+02;
0; Mismatches 0;
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43..1689
/*tag= a
/product= "GnT-IVb enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Pages 70-74; 112pp; Japanese.
0.6%; 5cc-
100.0%; Pre
0; 7
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                                                                                                                                       1112 agggagtggcagagga 1128
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         Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KIRI ) KIRIN BEER KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oguri S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-348516/30.
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12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                V38385;
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Human; HCDR-1; HCDR-2; HCDR-3; human cell division regulator; apoptosis; inflammation; cell proliferation disorder; adenocarcinoma; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes human cell division regulator (HCDR) 1. HCDR proteins are active in interphase, and are used for the treatment or prevention of inflammation and disorders associated with cell proliferation and apoptosis. HCDR may be administered to a patient having a disorder associated with an increase in apoptosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such a disorder may be e.g. neurodeficiency, a neurodegenerative disease, aplastic anaemia, an ischaemic injury, liver damage, or viral infection such as hepatitis B or C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                  Human cell division regulator; HCDR; interphase; inflammation; cell proliferation; apoptosis; neurodeficiency; neurodegenerative disease; ablantic anaemia; ischaemic injury; liver damage; viral infection; hepatitis B; hepatitis C; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1816 BP; 494 A; 473 C; 494 G; 355 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                 Shah P;
                                                       DNA encoding human cell division regulator (HCDR) 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                      Cell division regulators active in interphase
                                                                                                                                                                                                                                                                                                                                                 Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1. Mismatches
                                                                                                                                                                                                                                                                                                                                                 Corley NC, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1A-E; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X01577 standard; DNA; 1818 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human HCDR-1 coding sequence.
                                                                                                                                                                                                                                             98US-0165234.
                                                                                                                                                                                                                                                                        97US-0951148.
98US-0165234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 ggaaacttcttggtgct 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-1999 (first entry)
                            13-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-429499/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; Y23782.
                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                             01-OCT-1998;
                                                                                                                                                                                                                                                                        15-OCT-1997;
01-OCT-1998;
                                                                                                                                                                                      US5928899-A.
                                                                                                                                                                                                                  27 - JUL - 1999
                                                                                                                                                                                                                                                                                                                                                 Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x01577;
X85940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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Gaps

Length 1724; Indels 0;

0.6%; Score 17; DB 19; I ilarity 100.0%; Pred. No. 1.7e+02; Conservative 0; Mismatches 0;

Ouery Match Best Local Similarity Matches 17; Conserva 1341 agggagtggcagaggga 1357 |||||||||||||||||

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The present sequence is the coding sequence of human TRAF four associated factor TRAF2. The gene was discovered by screening a human placenta cDNA library using a two-hybrid system. The protein associates with the TRAF domain located at the carboxyl-terminal of TNF seceptor associated factor 4 (TRAF4), which is believed to be an orcoprotein. Antibodies that bind to TNF four associated factors (TRAFs) may be used to treat or diagnose tumours (e.g. breast cancer) when alsothogo at an appropriate drug, precursor or enzyme. Antagonists, and matisense sequences of TRAFs may be used to treat cancers. TRAF proteins, antibodies that recognise them and DNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitrite reductase; transgenic crop; transgenic tree; detoxification;
                                                                                                                                                                                                                                            Novel tumour necrosis factor receptor associated factor 4 associate factors useful for developing cancer screens, and treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1906 BP; 655 A; 320 C; 372 G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or them may be useful as tools for cancer research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= nitrite_reductase
                                                                                                (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14/c
T09084 standard; cDNA to mRNA; 2160 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/label= poly_A_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
40..1806
                                                                                                                                                                                                                                                                                                        Claim 4; Page 47-50; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Sco
ilarity 100.0%; Pi
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Populus nigra L. var italica
                 98CA-2245340
                                                          98CA-2245340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2796 gtttttaaagaagtctt 2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367.390
/*tag= b
                                                                                                                                     Toji.S, Tamai K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2114 . . 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2146..2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atmospheric pollutant; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    838..860
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nitrite reductase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                2000-351124/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                   P-PSDB; Y94209
                 19-AUG-1998;
                                                          19-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP07236486-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_signa!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer_bind
                                                                                                                                       Yano M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T09084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 63
This sequence encodes the human cell division regulator-1 (HCDR-1) protein of the invention. Polynucleotides complementary to the HCDR-1 coding sequence can be used as probes to detect the DNA in a sample. The polynucleotide sequences encoding HCDR may be used to prevent/treat inflammation and disorders associated with cell proliferation and apoptosis and in assays that detect activation of cancers. Polynucleotides encoding HCDR may be used for the diagnosis of conditions associated with expression of HCDR, including disorders associated with cell proliferation/apoptosis e.g. adenocarcinoma and AIDS. The polynucleotides may also be used in Southern or Northern analysis, dot blot, or other membrane based technologies; in PCR technologies; or in dipstick, pin, or ELISA assays or microarrays utilising fluids or tissues from patient biopsies to detect altered HCDR expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFAF2; TRAF four associated factor 2; tumour formation; breast cancer; TRAF4; TNF receptor associated factor; tumour diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding human cell division regulators (HCDR) - useful for diagnosing, preventing and treating inflammation and disorders associated with cell proliferation and apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 20; Length 1818;
Pred. No. 1.7e+02;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TRAF four associated factor TFAF2 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1818 BP; 494 A; 473 C; 494 G; 355 T; 2 other;
                                                                                                                                                                                                                                                                 Shah P;
                                                                                                                                                                                                                                                                 Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A15550 standard; cDNA to mRNA; 1906 BP.
                                                                                                                                                                                                                                                                 Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= TFAF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 1; 59pp; English
                                                                                                                                         97US-0951148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.68;
                                                                                                                                                                                97US-0951148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      719 ggaaacttcttggtgct 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              804 ggaaacttcttggtgct 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                           (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                 Bandman O, Corley NC,
                                                                                                                                                                                                                                                                                                      WPI; 1999-166646/14.
P-PSDB; W73971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA2245340-A1.
                   Homo sapiens
                                                                                                                                         15-OCT-1997;
                                                                                                                                                                                  15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                          US5871973-A
                                                                                                  16-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-2000
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A15550;

Key

.ESULT 62 .15550/c

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Gaps

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Length 1906; 0; Indels

Score 17; DB 21; I Pred. No. 1.7e+02; 0; Mismatches 0;

Baughn MR;

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The present cDNA sequence encodes human epidermal protein-6 (HEPI). The cDNA clone is derived from PTHYNOT03 library which was constructed using fenal scolated from left parathyroid tissue of a 69-year-old caucasian female during a partial parathyroidectomy. Recombinant vectors comprising HEPI cDNA are introduced into host cells for protein expression. The HEPI proteins are useful for the treatment of epithelial disorders, including dyshidrotic cozema and scabies, cell proliferative disorders including actinic keratosis and arteriosclerosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour rejection antigen; vaccine; cancer; E antigen precursor gene; ss.
                                                                                                                        New human epidermal proteins (HEPI-1) to (HEPI-6) useful for the diagnosis, treatment and prevention of epithelial, cell proliferative, and autoimmune inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                  proteins are useful for treating disorders associated
                                                                                                                                                                                                                                                                                                                                                                            autoimmune/inflammatory disorders like acquired immune deficiency syndrome (AIDS) and Addison's disease. Pharmaceutical compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 21; Length 2284; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumour rejection antigen is useful as a vaccine against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lurquin C, Traversari C; P, Van Pel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
               Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2284 BP; 452 A; 775 C; 534 G; 523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
               Guegler KJ,
                                                                                                                                                                                             Claim 7; Page 78-79; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boon T, Chomez P, De Plaen E,
Van Den Eynde B, Van Der Bruggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
               Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0705702.
91US-0728838.
91US-0764365.
91US-0807043.
                                                                                                                                                                                                                                                                                                                                                                                                                                     with altered HEPI expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0142368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0142368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2262 CAGGAAGGGCTGAGAT 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1881 caggaagggctgagat 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E antigen precursor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X84103 standard; DNA;
                                                                   2000-195295/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-418294/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancerous diseases
               Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                    comprising HEP1
                                                                                    P-PSDB; Y44989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5925729-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1991;
09-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1991
12-DEC-1991
               Tang YI,
Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               x84103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
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ID X8
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                                                                                                                                                                                                                                                                                The gene encodes a nitrite reductase gene isolated from Populus nigra. The gene is useful in generation of street trees with a high power for clarfiying NO2, an atmospheric pollutant. The gene can also be used in transgenic plants, esp. crops, bred to contain less nitrosamines (a carcinogenic substance present in food).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dyshidrotic eczema; cell proliferative disorder; actinic keratosis; arterioscierosis; aucoimmune disorder; inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; antiHIV; dermatological; anitarterlosclerotic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                           Nitrite reductase gene from Populus nigra - useful for breeding
trees to remove nitrogen di:oxide from the atmosphere or for crops
which produce fewer carcinogenic nitrosamine(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epidermal protein-6; HEPI; epithelial disorder; scabies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mature human epidermal protein-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 16; Length 21
Pred. No. 1.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2160 BP; 660 A; 388 C; 570 G; 542 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human epidermal protein-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
47..1636
                                                                                                                                                                                                                                                  Claim 1; Page 5-8; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2/c
250582 standard; cDNA; 2284 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human epidermal protein-6 cDNA
                                                  94JP-0032359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0155203.
               94JP-0032359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcttgccaagtatcttg 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 GCTTGCCAAGTATCTTG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
148..1636
/*tag= c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                      (TOYT ) TOYOTA JIDOSHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                        WPI; 1995-347454/45.
P-PSDB; R87973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200006727-A2
               02-MAR-1994;
                                                  02-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1999;
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07-DEC-1998;
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Gaps

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Query Match
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                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                072476
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SSXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes the stable antigen E. This antigen is expressed along with antigens "D. F and A" by the human melanoma cell line MZ2-MZE. These antigens are all recognised by cytolytic T cells. A subline of MZ2-MZE. MEL3 Which only expresses antigen E. This cell line was chosen as a source for the isolation of this sequence. This sequence was found to contain three exons. The open reading frame for antigen E was contained within the first two exons. An ArG is, located at position 66 of exon 3 and is followed by an 828 base pair reading frame. The three exons contain 65, 73 and 1551 base pairs. During the isolation of this sequence two different but closely reated CDNAs were also identified. These cDNAs, when tested, did not transfer expression of antigen E, but they did show substantial homology to the antigen E cDNA sequence. These new cDNAs represent a
                                                   This sequence represents the E antigen precursor gene. The invention relates to a tumour rejection antigen sequence that is useful as a tumour rejection antigen for vaccination against cancerous
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stable; antigen; E; D; F; A; human; melanoma; cell line; MZ2-WEL; cytolytic T cell; MEL3.1; open reading frame; homology; MAGE; melanoma antigen; ss.
                                                                                                                                                                                                                               ö
                                                                                                                                                                                            Length 2418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid mol. encoding a human tumour rejection antigen precursor - useful as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Traversari C;
                                                                                                                                                                                                                               0; Indels
                                                                                                                                          Sequence 2418 BP; 562 A; 582 C; 675 G; 599 T; 0 other;
                                                                                                                                                                                            Score 17; DB 20; I
Pred. No. 1.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boon I, Chomez P. De Plaen E, Lurquin C, Tra
Van Den Eynde B, Van Der Bruggen P, Van Pel A;
                Example 20; Column 15-18; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 69-70; 142pp; English.
                                                                                                                                                                                      0.6%;
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                        Q32351 standard; DNA; 2419 BP
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91US-0728838.
91US-0764364.
91US-0807043.
                                                                                                                                                                                                                                                                 1652 ggtcctgggcaccctgg 1668 [[[[]]]]]]]
                                                                                                                                                                                                                                                                                                  738 ggtcctgggcacctgg 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen E gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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12-DEC-1991;
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09-JUL-1991;
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                                                                                                          conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
new family of genes refered to as melanoma antigens (MAGE) (see also Q32352-69).
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour rejection antigen E; melanoma antigen-3; MAGE-3;
cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van DER BRUGGEN P;
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100.0%; Pred. No. 1.7e+02;
                                                                                                                                                           Length 2419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumour rejection antigen precursor MAGE3 - useful in treatment and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;
                                                                                     Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;
                                                                                                                                                                                 1.7e+02;
                                                                                                                                                         0.6%; Score 17; DB 13;
100.0%; Pred. No. 1.7e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaugler B, Van DEN EYNDE B,
                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour rejection antigen E encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 58; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leucocyte antigen (esp. HLA-A1).
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100.0%; Pit
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                                                                                                                                                                                                                                                                                                                                                                                                            Q72476 standard; DNA; 2419
                                                                                                                                                                                                                                                                                                739 ggtcctgggcacctgg 755
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                                                                                                                                                                                 Best_Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity 100.9
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-333192/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9423031-A
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T05086
ID T05086
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072472 is the tumour rejection antigen E precursor gene, another gene 072470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection antigen precursor. Melanomas characterised by the expression of MAGE-3 can be detected, or monitored, by contacting a test sample with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour antigen rejection precursor E; melanoma antigen-3; MAGE-3; cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van DER BRUGGEN P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the antigen E coding sequence. The invention relates to a tumour rejection antigen sequence useful as a tumour rejection antigen for vaccination against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 20; Length 2419;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                          New tumour rejection antigen is useful as a vaccine against
                                                                                                                                                                                                                Lurquin C, Traversari C;
P, Van Pel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumour rejection antigen precursor MAGE3 - useful treatment, and diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 37-40; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 20; Page 28; 105pp; English
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100.0%; Pre
                                                                                                                                                                                                                   Boon I, Chomez P, De Plaen E,
Van Den Eynde B, Van Der Bruggen
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                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q72472 standard; DNA; 2420 BP
94US-0142368.
91US-0705702.
91US-0728838.
91US-0764365.
91US-0807043.
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                     WPI; 1999-418294/35
                                                                                                                                                                                                                                                                                                                                                                                      cancerous diseases
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  02-MAY-1994;
23-MAY-1991;
09-JUL-1991;
23-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAR-1994;
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                                                                                                             12-DEC-1991;
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Q72472
     PRESENTATION OF STATE OF STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A gene sequence (T05086) hybridizes with a 2.4 kb fragment from human melanoma cell line MZ2-MEL but not with E- antigen loss variants of MZ2-MEL. This E precursor antigen gene sequence was obtd. from a cosmid derived from DNA of the E+ subclone MZ2-MEL 43.
                                                                                                                                                                                          Melanoma; MZ2-MEL; tumour rejection antigen; cancer; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determn. of cancerous condition(s) - using a nucleic acid as a primer to determine expression of a MAGE tumour rejection antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2419 BP; 560 A; 581 C; 677 G; 601 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 20; Page 69-70; 121pp; English.
                                                                                                                                    M22-MEL antigen E precursor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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94US-0204727.
94US-0209172.
94US-0299849.
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                                                                                    (first entry)
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1994;
                                                                                 26-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-1999
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01-MAR-1994;
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agent that can recognise MAGE-3. The melanoma can be treated by the administration of cytolytic T cells specific for the complex of antigen D (the mature rejection antigen derived from MAGE-3) and a human leucocyte antigen (esp. HLA-A1).
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours; HLA-restricted cytotoxic T-lymphocyte activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used to produce the C-terminal MAGE-1 peptides described in R70915 to R70969. These peptides are useful for defining epitopes that engender a HLA-restricted cytotoxic lymphocyte activity against MAGE-1 antigens. Compans. containing these peptides can be administered, as a vaccine to patients susceptable to MAGE
                                                                                                                                                          ö
                                                                                                                         Length 2420;
                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human melanoma antigen, MAGE-1, peptide(s) - useful for stimulating immune response against melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 other;
                                                                             Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 other;
                                                                                                                         0.6%; Score 17; DB 15;
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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626..1555
/*tag= a
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                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                            Human melanoma antigen MAGE-1.
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                                                                                                                                                                                                                      739 ggtcctgggcaccctgg 755
                                                                                                                                                                                                                                                                                                                                                             09-OCT-1995 (first entry)
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                                                                                                                           Query Match
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                              085435;
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095435
10 085435
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                 Human secreted protein gene 85 clone HSDFV29.
                                                          V59595 standard; DNA; 2503 BP.
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970S-0043689.
970S-0043670.
970S-0043672.
970S-0043672.
970S-0043674.
970S-0047500.
970S-0047500.
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97US-0047588.
97US-0047589.
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97US-0040163
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97US-0043313
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97US-0043576
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97US-0047582
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97US-0047584
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97US-0047586
739 ggtcctgggcaccctgg 755
                                                                                                          (first entry)
                                                                                                          06-JAN-1999
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                                                                                  V59595;
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Gaps

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Query Match 0.6%; Score 17; DB 16; Length 2420; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 17; Conservative 0; Mismatches 0; Indels (

1652 ggtcctgggcaccctgg 1668

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New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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le AM, Fischer CL, Florence RA, Greene JM, Hu JS;
eur DW, Li Y; Moore RA, Ni J, Olsen HS, Rosen CA;
i Y, Soppet DR, Young PE, Yu GL, Zeng Z;
970S-0047597.
970S-0047598.
970S-0047599.
970S-0047600.
970S-0047612.
970S-0047613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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97US-00
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Kyaw H, Lafleur DW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; W74815
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This sequence represents a nucleic acid molecule designated Gene 85 from the human cDNA clone HSDFY29 (deposited as clone ATCC 209076) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. V95502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 movel genes and their fragments (nucleic acid sequences: V59511-V58812; amino acid sequences W74731-W75025) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polyneclectides, correcting the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see V5911 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel human nucleic acid (cDNA) sequences (A), that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ы</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents ^{-1}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endometrium; human; tumour; cancer; anticancer; cytostatic; E
treatment; uterine; gene therapy; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                 Score 17; DB 19; Length 2503;
Pred. No. 1.7e+02;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        Sequence 2503 BP; 561 A; 705 C; 658 G; 568 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human endometrium tumour cDNA derived EST 116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (META-) METAGEN GES GENOMFORSCHUNG MBH.
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                                                                                                                                                                                                                                                                                                                                                                             0.6%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; Y60295, Y60296, Y60297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z42096 standard; cDNA; 2646 BP.
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ses 17; Conservative
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                                                                                                                                                                                                                                                                                     uses).
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Claim 1; Page 316-317; 721pp; English.

Endress GA;

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expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. Z41981-Z42121 represent EST fragments derived from a human endometrium tumour cDNA library which encode the protein sequences represented in Y59941-Y60328.
                                                                                                                                                                                                                                                                                                                                                                                                                          Neurodegenerative polypeptide; HHPDZ65; stroke; pain; epilepsy; therapy; neurodegenerative disease; ss.
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHPD265 polypeptide(s), their corresponding DNA, antibodies, agonists and antagonists - are useful in the treatment of stroke, pain, epilepsy and neurodegenerative diseases
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                                                                                                                                                           Length 2646;
                                                                                                                                                                                     Indels
                                                                                                                  Sequence 2646 BP; 787 A; 502 C; 546 G; 811 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    Neurodegenerative polypeptide HHPDZ65 coding sequence.
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                                                                                                                                                         Score 17; DB 20; I
Pred. No. 1.7e+02;
0; Mismatches 0;
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                                                                                                                                                 0.6%; Sur-
100.0%; Pre
0; /
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97GB-0008936.
97EP-0310289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-559436/48.
P-PSDB; W80315.
                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
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01-MAY-1997;
18-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                           V68056;
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repression/expression of foreign genes by oxygen/formate;

N81166 standard; DNA; 2971 BP

N81166/c

29-OCT-1990

N81166;

fdhF gene

synthetic

1879 cacggtccccaggagg 1895

2624 cacggtcccccaggagg 2640

Location/Qualifiers

749..2896

Key

/*tag= a /product=fdhF 737..740 /*tag= b

RBS

88EP-0105219

30-MAR-1988; 31-MAR-1987; 09-OCT-1987;

05-OCT-1988 EP285152-A.

87DE-3710633 87DE-3735381

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                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA contg a consensus sequence common to genes that are repressible by oxygen and inducible by formate under anaerobisc conditions and the fdhF promoter used as a simple expression system for foreign genes. Expression does not require temp shifts or addition of inducers. (Formate is produced naturally by microorganisms in the late, anaerobic growth phase).
                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA contg consensus sequence and specific promoter providing foreign gene repression under anaerobic conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 17; DB 9; Length 2971;
.00.0%; Pred. No. 1.7e+02;
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Best Local Similarity 100.0
Matches 17, Conservative
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                                                                                                                                                                                                                                                                                                             Birkmann A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               013115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 76
Q13115
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invention. HHPDZ65 is useful for the treatment of stroke, pain, epilepsy, neurodegenerative diseases and others. The DNAs and proteins are useful in a method for screening to identify compounds which stimulate or inhibit the function of the HHPDZ65 proteins. The polypeptides are useful in a process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the HHPDZ65 polypeptides.

Sequence 2711 BP; 559 A; 820 C; 852 G; 478 T; 2 other;

Query Match 0.6%; Score 17; DB 19; 1 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 17; Conservative 0; Mismatches 0;

Gaps

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Indels

Length 2711;

This sequence encodes the HHPD265 neurodegenerative polypeptide of the

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This polynucleotide comprises clone pA1276 that codes for human T-cell surface antigen CD97 (see W48756). It was isolated from a T-cell library enriched for mitogen-induced genes. The invention relates to the previously unrecognised alpha subunit of CD97 that acts in the establishment and maintenance of inflammation. Soluble CDD97 acts as an adhesion factor for endothelial cells and smooth muscle cells, implicating it as a modulator of atherosclerosis. CD97 alpha also acts as a motility factor to cells bearing the alpha(V)beta-3 receptor, indicative of a role in angiogenesis. CS9luble CD97 alpha1, alpha2, and alpha3 subunits (having different combinations of EGF repeats) all originate as a proprotein with the beta subunit (see W48756). Host cells transfected with a nucleic acid encoding a CD97 alpha subunits are claimed. CD97 alpha subunit polypeptides, nucleic acids, antibodies and antagonists (e.g. CD97 subunit antisense nucleic acids) are used in claimed methods for: determining the degree of inflammation and site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibiting atheroslerosis; and treating or inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 7-transmembrane receptor; lectomedin; lectin-binding; mucin; olfactomedin; cellular adhesion; atherosclerosis; gene therapy; vascular disease; CD97; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compounds that inhibit soluble CD97 alpha subunit inhibiting anglogenesis associated with chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3156;
                                                                                                                                                                                                                                                                                                                                                                   New soluble CD97 alpha subunit isoform(s) - used to develop products for the detection and treatment of inflammation, atherosclerosis and angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3156 BP; 652 A; 973 C; 860 G; 671 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 17; DB 19; I
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compounds that inhibi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CD97 protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z27969 standard; DNA; 3156 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD97 associated inflammation.
                                                                                                                                                                  97WO-US19772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1336 ccaggagggagtggcag 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2683 ccaggagggagtggcag 2699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z27969;
05-JAN-2000; (first entry)
49..99
/*tag= b
100..2553
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                               WPI; 1998-261492/23.
P-PSDB; W48756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation;
                                                                                                                                                                  24-OCT-1997;
                                                                                           WO9817796-A2
 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identifying
                                        mat_peptide
                                                                                                                                30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression;
                                                                                                                                                                                                                                                                             Kelly K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
227969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Overlapping clones which make up this sequence were isolated from a mouse Peripheral Blood Lymphocyte lambda gt10 cDNA library. The protein encoded by this sequence is purified and can mediate the cytolytic activity of mammalian cells. It specifically distinguishes tumour cells making it a candidate for the development of products for the immunodetection and immunotherapy of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell surface antigen; CD97; human; inflammation; angiogenesis; atherosclerosis; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding a natural killer cell receptor – used to develop prods. for the immuno-detection and immuno-therapy of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3000;
                                                         NK; cytotoxic drugs; tumour cell; immunotherapy; mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3000 BP; 997 A; 661 C; 716 G; 626 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Le
1.7e+02;
thes 0;
                     Encodes partial murine Natural Killer receptor.
                                                                                                                                                                                                                                       /product= murine NK receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 1
Pred. No. 1.7e
0; Mismatches
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49..2556
/*tag= a
                                                                                                                                ocation/Qualifiers
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/note= "partial"
22..2946
/*tag* h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Scilarity 100.0%; P
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CD V18471 standard; CDNA; 3156 BP.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) NAT INST OF HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ortaldo J, Young H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-245694/33.
P-PSDB; R13320.
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also 013114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                    08-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-1990;
                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1998
                                                                                                                                                                                                                                                                           US7535206-A.
                                                                                                                                               sig_peptide
                                                                                                                                                                                                      mat_peptide
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Gaps

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V18471;

Key

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Overexpression of nitrate reductase (NR) can stimulate the early development of plants, shortening the duration of the vegetative phase and causing earlier germination, flowering and ripening by about two weeks. Overexpression of NR can also cause the level of nitrate stored in a plant to be reduced, reducing risks to health and also possibly improving organoleptic qualities. The NR gene was tuncteduced into plants by transforming a strain of Agrobacterium tunmefaciens with a plasmid and using it to infect the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus protein; chordin; dorsal tissue; neural tissue; vertebrate; endodermal differentiation; treatment; neurodegenerative disease; nerve cell; transforming growth factor; TGF; secreted protein; ss
                                                                                                                                                                                                                                                                                                      Inducing over-expression of nitrate reductase in plants - esp. by incorporation of foreign gene, for stimulating early development and reducing nitrate accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%; Score 17; DB 14; Length 34
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3457 BP; 1014 A; 700 C; 752 G; 991 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "hydrophobic signal peptide"
/note= "hydrophobic signal peptide"
/*tag= c
/note= "putative secreted protein"
                                                                                                                                                                               Chupeau Y, Dorlhac F, Morot-gaudry J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297..3122
/ktag= a
/product= Xenopus_protein_chordin
297..353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus frog protein "chordin" encoding cDNA.
                                                                                                                                            (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Figure 3; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T93499 standard; cDNA; 3796 BP.
                                                          93WO-FR00222.
                                                                                                   92FR-0002658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           909 gaaggaagagagatttt 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
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                                                                                                                                                                                                                                              WPI; 1993-303468/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis.
                                                                                                                                                                                                                                                                 P-PSDB; R41757
                                                          05-MAR-1993;
                                                                                                   05-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5679783-A.
                 16-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-1997
                                                                                                                                                                                   Caboche M,
Vincentz M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T93499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T93499
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides purified and isolated human 7-transmembrane receptor lectomedin polypeptide or its fragments. The lectomedin polypeptide comparises extracellular lectin-binding, olfactomedin-like and mucin-like domains. The polypeptide can be produced by standard recombinant methodology. The polypeptide is involved in callular adhesion and cytoplasmic metabolic pathways that are modulated by extracellular signaling. Specific binding to lectomedin-l expressed on smooth muscle cells may be required for proliferation of these cells in atherosclerosis. The polypeptide is used to raise specific antibodies, and to identify specific binding agents that modulate (increase or decrease) its activity. The lectomedin nucleic acids are used as source of probes and primers, and of therapeutic antisense, ribozyme or triplex-comming agents, and in gene therapy to restore deficient lectomedin activity. Specific binding agents of lectomedin are are used for treating diseases that involve lectomedin activity, e.g. vascular diseases such as atherosclerosis. The present sequence represents the DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                    New human lectomedin receptor polypeptide, used to identify specific binding partners for treating e.g. vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nitrate reductase; germination; flowering; ripening; development; growth stimulation; Agrobacterium tumefaciens; nitrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 17; DB 20; Length 3156;
100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3156 BP; 651 A; 974 C; 860 G; 671 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a //product= Nitrate reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 106-110; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitrate reductase Nia2 gene derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
144..2858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i8/c
Q48468 standard; cDNA; 3457 BP.
                                                                                                                         99WO-US04676.
                                                                                                                                                                98US-0076782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0
Watches 17; Conservative
                                                                                                                                                                                                                                                                                       WPI; 1999-571596/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human CD97 protein.
                                                                                                                                                                                                         (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                               P-PSDB; Y41090.
Homo sapiens
                                                                                                                                                                04-MAR-1998;
                                                                                                                       04-MAR-1999;
                                                                                                                                                                                                                                                Hayflick JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana sp
                                         WO9945111-A1
                                                                                10-SEP-1999
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755ULT 248468/ 75 04

Key

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Gaps

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Length 3457;

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Gaps
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                                                                                                                                                                                                                                                                                          promoter of fast-growing Rhizobium japonicum - used to drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colon carcinoma kinase 4; CCK-4; receptor tyrosine kinase; signal transduction; colon cancer; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                           transcription in rhizobium of heterologous structural genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4216 BP; 906 A; 1254 C; 1251 G; 793 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 8; Ler
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon carcinoma kinase 4 (CCK-4) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cocation/Qualifiers
193..3405
                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.0°,
100.0%; Piv
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T45351 standard; cDNA; 4258 BP
                                                                                                                        85us-0763800.
                                                                                       86EP-0306105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3903 agctcaacctcatccac 3919
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                                                                                                                                                              (LUBR.) LUBRIZOL GENETICS (LUBR.) LUBRIZOL GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
271..3402
/*tag= c
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                                                                                                                                                                                                                                                      WPI; 1987-051801/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                   Appelbaum ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-1997
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                                                                                       07-AUG-1986;
                                                                                                                          07-AUG-1985;
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                                                   25-FEB-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
               EP211661-A.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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ö
                                                                                                                                                                                                                                                                                                       This cDNA encodes a Xenopus protein "chordin". The functional recombinant protein chordin has a defined sequence of 941 amino acids and can induce dorsal and neural development and endodermal differentiation in vertebrates. The presence of a hydrophobic signal sequence, four possible N-glycosylation sites and conserved Cys-rich repeat regions suggest that chordin is a secreted protein. The DNA sequence can be operatively linked with an expression vector, to form a construct and a transformant can be obtained by introducing the construct into a host. Chordin may be useful as a component of culture media for culturing cells such as nerve or muscle cells, for treating neurodegenerative diseases and damaged nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                  DNA encoding Xenopus frog protein - that induces dorsal and neural development and endodermal differentiation in vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of nitrogen fixation gene H (nifH) promoter and coding region and the nifH-nifD intergenic region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3796 BP; 1046 A; 841 C; 958 G; 951 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium expression vector; plant expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18; Le
1.7e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 1; Pred. No. 1.7e 0; Mismatches
                                                                                                                                                                                                                                                                   Claim 1; Columns 19-22; 27pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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/note= "claimed"
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ilarity 100.0%; P.
Conservative 0;
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/label= nifD
1770..2023
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                                                   94US-0343760
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/*tag= c
2024..2914
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1933..1936
/*tag= b
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                                                                                                                          De Robertis EM, Sasai Y;
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P-PSDB; W31559.
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Best Local Similarity
Matches 17; Conserv
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               22-NOV-1994;
                                                   22-NOV-1994;
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promoter
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N70558
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The present expanded cDNA sequence encodes human BAG-5 (Bcl-2 associated athanogene-5) protein. BAG is a Hsc70/Hsp70-regulating protein protein the protein bloactivity, degradation, complex assembly/disassembly and translocation across membranes). It competes with Hip for binding to the Hsc70/Hsp70 APPase binding domain and promotes substrate release. Gene transfection studies indicate that BAG proteins influence a wide variety of cellular phenotypes through their interactions with Hsc70/Hsp70, proliferation, enhancing tumour cto apoptosis, promoting cell proliferation, enhancing tumour cell migration and metastasis and altering transcriptional activity of steroid hormones. BAG also stimulates Hsc70-mediated adenosine triphosphate (AFP) hydrolysis by
proliferation, cell migration and metastasis and steroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                           Length 4308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fanconi Anemia Group C; FACC; complementing cDNA; varient; open reading frame; diagnosis; Fanconi anemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                   Sequence 4308 BP; 1201 A; 897 C; 987 G; 1222 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 17; DB 21; I
100.0%; Pred. No. 1.7e+02;
tve 0; Mismatches 0;
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174..1850
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                                                      Claim 12; Fig 17; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           0.0%,
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                    accelerating ADP/ATP exchange.
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/*tag= b, 3042..30*
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92US-0918313.
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3163..3175
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3289..3322
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3323..4455
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                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 0.69
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human FACC cDNA clone #1.
                 receptor function
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21-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         051426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                       New isolated receptor tyrosine kinase, CCK-4 - used for developing prods. for the diagnosis and treatment of CCK-4 signal transduction disorders, partic. colon cancer
                                                                                                                                                                                                                  A cDNA sequence (T45351) codes for a novel human receptor tyrosine kinase, colon carcinoma kinase-4 (W08747), or CCK-4, which is preferentially expressed in cancerous colon tissue, compared with normal colon. The cDNA sequence is a consensus of 6 overlapping CDNA clones isolated from a human placenta library using primers based on conserved motifs of protein tyrosine kinase catalytic domains. CCK-4 nucleic acids can be used in the prodn. of recombinant CCK-4 polypetides, and as probes in the diagnosis and screening of CCK-4 signal transduction disorders, esp. colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAG-1 related proteins from humans, Caenorhabditis elegans and Schizosaccharomyces pombe useful for modulating tumor cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 17; DB 18; Length 4258; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Full length expanded cDNA sequence for human BAG-5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4258 BP; 868 A; 1252 C; 1282 G; 856 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Human BAG-5 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 247..1590
                                                                                                                                                                                     Claim 1; Fig la-d; 129pp; English.
                 Ullrich A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z51806 standard; cDNA; 4308 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US21053
                                                                                                                                                                                                                                                                                                                                                                                              cancer, and in gene therapy
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BURN-) BURNHAM INST
                 Alves F, Mossie K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-256937/22.
P-PSDB; Y70517.
                                                    WPI; 1997-021219/02
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                                                                        P-PSDB; W08747
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51806
10 Z51806
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This cDNA clone includes a coding region for human Fanconi anaemia complementation group C (FAC, see W68546), a protein that modulates approposis in haematopoietic progenitor cells (HPC). The invention provides conjugates, including fusion proteins, comprising FAC and a targetting molecule which binds to a cell surface protein of the HPC and is internalised. Such targetting molecules include interleukin-3 (see W68547) and antibodies which recognise CD33 (see W68548-49). The conjugate, or a nucleic acid encoding it, can be used to deliver FAC to an HPC, specifically to inhibit apoptosis, particularly in patients exposed to high doses of chemotherapy for treatment of non-myeloid cancers, also to treat Fanconi anaemia (by complementation of the genetic defect). Treatment of HPC is done in vitro, ex vivo (e.g. for recombinant production of conjugate in cell cultures) or in vivo. Treatment with FAC may eliminate the need for extensive bone marrow transplants to restore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid mol. encoding a human tumour rejection antigen precursor - useful as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4567 BP; 1080 A; 1135 C; 1177 G; 1175 T; 0 other;
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100.0%; Pred. No. 1.7e+02;
1ve 0; Mismatches 0;
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Van Den Eynde B, Van Der Bruggen P, Van Pel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
3881..4711
/*tag= a
             Claim 6; Page 40-45; 72pp; English
                                                                                                                                                                                                                                                                                                                                             naematopoiesis after chemotherapy.
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91US-0728838.
91US-0764364.
91US-0807043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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09-JUL-1991;
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Q32352
ID Q3
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                                                                                                                                                                                                                                                                                                 The sequences given in Q51426-28 represent cDNA varients from the Fanconi Anemia Group C Complementing (FACC) cDNA. These three cDNA molecules are cellular varients of a single cDNA transcribed from the same gene. The three cDNAs each contain an identical open reading frame encoding the FACC protein. The FACC protein may be used for the diagnosis and study of Fanconi anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New conjugate of Fanconi anaemia molecule and peptide selective for haematopoletic precursor cells - inhibits apoptosis of these cells, for treating Fanconi anaemia and patients undergoing high-dose chemotherapy for cancer
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bone marrow; chemotherapy; gene therapy; human; ds.
                                                                                                                                                                          Human cDNA which complements Fanconi Anaemia gp. C - used to develop prods. for use in diagnosis, study and therapy of Fanconi Anaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 14; Lengtn 4*.: Pred. No. 1.7e+02;
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                                                                                             Strathdee CA, Wevrick R;
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0; Mismatches
                                   HOSPITAL FOR SICK CHILDREN.
UNITED MEDICAL & DENTAL SCHOOL GUYS.
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256..1929
/*tag= a
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93US-0003963.
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                                                                                           Mathew CG,
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P-PSDB; W68546.
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P-PSDB; R44139.
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15-JAN-1993;
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                                                                                           Buchwald M,
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RESULT 133945

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Query Match
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ID T42117
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X84113
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                     The sequences given in 032352-69 represent a new family of genes refered to as melanoma antigens (MAGE). The cDNAs of this gene family were identified during the isolation of the antigen E gene. The MAGE CDNAs, when tested, did not transfer expression of antigen E, but they did show substantial homology to the antigen E cDNA sequence. The MAGE DNAs share a certain degree of homology with each other and are expressed in tumour cells including several types of human tumor cells as well as in human tumors. MAGE expression is not restricted to melanomas. MAGE refers to a family of tumor rejection antigen precursors. The antigens resulting from these genes are referred to as MAGE TRAS or melanoma antigen tumor rejection antigens. See also Q32351.
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DER BRUGGEN P;
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cancer; cytolytic T cells; antigen D; human leucocyte antigen;
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Pred. No. 1.7e+02;
0; Mismatches 0;
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Disclosure; Page 71-73; 142pp; English.
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100.0%; Pre
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nes 17; Conser
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Best Local &
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CDS
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This sequence represents the MAGE-1 gene sequence. The invention relates to a tumour rejection antigen sequence that is useful as a tumour rejection antigen for vaccination against cancerous
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mature rejection antigen derived from MAGE-3) and a human leucocyte antigen (esp. HLA-A1).
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                                                                                                                              Length 5674;
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A;
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                                                                 Seguence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other,
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100.0%; Pred. No. 1.7e+02;
:ive 0; Mismatches 0;
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Van Den Eynde B, Van Der Bruggen P, Van Pel
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                                                                                                               0.6%; Scor.
100.0%; Pre
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91US-0728838.
91US-0764365.
91US-0807043.
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Best Local Similarity 100.
Matches 17; Conservative
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Matches 17; Conservative
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12-DEC-1991
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ote= "GGGAGCGGGATCAAC insertion in genomic DNA"
88..3489
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/note- T in genomic sequence"
5013..5153
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/note- "Region identical to plc-21 transcript"
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"AAC in genomic sequence"
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note= "Deleted in genomic DNA"
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|ote= "Intron-7 splice site"
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note= "intron-5 splice site"
104..3805
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note= "Intron-4 splice site"
25..3726
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ote= "Intron-3 splice site'
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                                                                                    Lats gene; large tumour suppressor; Drosophila melanogaster; fruitfly; polyadenylation site; protein serine/threonine-kinase; cell proliferation; antisense; dominant-negative; cancer; degeneration disorder: trauma; growth deficiency; therapy; antitumour; vulnerary; diagnostic; transgenic plant; transgenic animal; growth; senescence; ds.
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note= "A in genomic sequence"
92..5720
*tag= d
note= "Sequence from clone cDNA-A2"
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note= "Sequence from clone cDNA-9"
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note= "GGA in genomic sequence"
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note= "G in genomic sequence"
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note= "Intron-2 splice.site"
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                                                              Lats gene encoding large tumour suppressor.
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                                    22-JAN-1997 (first entry)
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                                                                                                                                                                           Drosophila melanogaster.
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             T42117;
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The present sequence is a DNA encoding Drosophila Lats (large tumour suppressor) protein which is a cell overproliferation inhibitor and angative regulator of cell cycle-dependent kinase cdc2/cyclin A. The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, metaplasia, or dysplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferrably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soff tissue sarcomas and ovarian tumours, and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity
Fruit fly; Lats; large tumour suppressor; cytostatic; vulnerary; cell overproliferation inhibitor; cdc2; cell cycle-dependent kinase; treatment; prevention; screening; cancer; skin; ovarian tumour; soft tissue sarcoma: pituitary disorder; gene therapy; hyperplasia; llf; luteinizing hormone hypogonadotropic hypogonadism; metaplasia; dysplasia; degenerative disorder; growth deficiency; physical trauma; hypoproliferative disorder; lesion; wound; lats knock-out mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                         region is identical to the 1-141 of Drosophila plc-21 transcript"
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00.0%; Pred. No. 1.7e+02;
ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fei X, Fukumoto RK, Zhang
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                                                                                                                                                                                                                                                                      "Lats protein
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1103..4402
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                                                                                                                                                                                                                                                                                                                                                                                              nucleotides of
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/note= "This
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Stewart RA;
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9803-0096997
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Matches 17; Conservative
                                                                                                                                                                    Drosophila melanogaster.
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P-PSDB; Y70393.
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Turenchalk GS,
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18-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/note- "AAAAGCAAATTAATAAAT in genomic sequence"
5657..5663
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/note= "GTGGCCCCCTCCCTCCTCAT in genomic
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100.0%; Pred. No. 1.7e+02;
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/note= "TGTAATTAGTG in genomic sequence"
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/note= "Deleted in genomic DNA"
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5151..5
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WO9630402-A1

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BERKANCE SKRAGARUK KUREERAAGGGGGGGGG

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Gaps

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21-JUN-2000

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355ULT 51508 70 Z51

Query Match

Matches

3

98802;

91

RESULT 198902

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Sequences of three polymorphic human NAT genes are given in Q48767-Q48772. Detection of polymorphic human NAT genes allows diagnosis of adverse effects to be caused by amino-contg. aromatic substances
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic human arylamine N-acetyl-transferase genes - used to diagnose adverse effects caused by amino-contg, aromatic
                                                                                                Arylamine N-acetyl-transferase; NAT; polymorphism; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6464 BP; 2087 A; 1189 C; 1282 G; 1906 T; 0 other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TOKM-) TOKYO METROPOLITAN INST. NEUROSCIENCES. (TOKY-) ZH TOKYOTO SHINKEIKAGAKA SOGO KENKYUSHO.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinoshita M,
                                            Arylamine N-acetyl-transferase type 3.
                                                                                                                                                                                                                        Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 37-41; 54pp; English.
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V52165
ID V52165 standard; DNA; 10240 BP.
                                                                                                                       amino; aromatic substance; ds
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717..1936
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1794..1799
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1800..1805
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21-APR-1994 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.
Matches 17; Conservative
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P-PSDB; R41246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1992;
                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP562547-A.
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                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                           Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a //product= Tumour rejection antigen MAGE-1.
/product= The CDS is not indicated in the text of the specification but is suggested in the layout of the sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to MAGE-1 - useful for hybridomas, recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A monoclonal antibody directed against the tumour rejection antigen (MAGE-1) can be used to detect MAGE-1 in samples by standard immunoassay methods for diagnosis and monitoring of cancer etc. The monoclonal antibody is designated MA454 and is produced by the hybridoma deposited as ATCC HBB11540. The monoclonal antibody is specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3. Peptide fragments of MAGE-1 (see R80618-20) may be useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide fragments of MAGE-1 (See R80618-20) may be useful as immunogens for production of the monoclonal antibody and antisera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5724;
                                                                                                                                                                                                                                               antigen; MAGE-1; monoclonal antibody; MAb;
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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SLOK ) SLOAN KETTERING INST CANCER RES.
(SLOK ) MEMORIAL SLOAN-KETTERING CANCER CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New monoclonal antibody binding specifically diagnosis and monitoring of cancer, also new MAGE-1 and immunogenic peptide(s)
                                                                                                                                                                                                Tumour rejection antigen (MAGE-1) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 16-19; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
3881..4711
                                                                                                                                                                                                                                                                         diagnosis; immunoassay; cancer; ss.
                                            Q98902 standard; DNA; 5724 BP
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Best Local Similarity
Matches 17; Conserv
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DB 14; Length 6464; 1.7e+02; hes 0; Indels

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Location/Qualifiers
301..360
/*tag= a
./note= 'these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for Tr pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                 New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                 X20500-21243 represent polynucleotide sequences from the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10461 BP; 2325 A; 3411 C; 2493 G; 2213 T; 19 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of biosynthetic products such as enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus contig SEQ ID #364.
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 491-497; 1150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V74675 standard; DNA; 10813 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                               98WO-US13041.
                                                                                                        97US-0050667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6768 geggeaectgegeaege 6784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 gaggaacetgagaaga 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-1999 .(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxic shock syndrome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus, aureus.
                                                                                                                                                                                                                                          WPI; 1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                               23-JUN-1998;
                                                                                                      24-JUN-1997;
                    30-DEC-1998
                                                                                                                                                                                                 Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
V74675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded to nit, or a repersentative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus procumbinate. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced py a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequences: the computer readable medium can be used in a computer-based system for identifying fragments of the submoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Produces from the present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in diagnosis kits and assays, and pharmaceutical vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                          Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 19; Length 10240;
Pred. No. 1.7e+02;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10240 BP; 2865 A; 1914 C; 2390 G; 3068 T; 3 other;
                                                                                                                                                                                                                      Fannon M;
                                                                                                                                                                                                                      Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 326-332; 1409pp; English.
                                                                                                                                                                                                                      Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08; Fix
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                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X20553 standard; DNA; 10461
                                                                                      97WO-US19588.
                                                                                                                                 96US-0029960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1947 gatttggaagagtttca 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7643 gatttggaagagtttca 7659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                   Choi GH,
Rosen CA;
                                                                                                                                                                                                                                                                                      WPI; 1998-272225/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention can be
WO9818931-A2
                                                                                      30-0CT-1997;
                                                                                                                               31-OCT-1996;
                                           07-MAY-1998
                                                                                                                                                                                                                      Barash SC,
Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae
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ZXQXmXmXmXxxHPXxxXnHeexxmXnSeeclannoonnnoonnnoonn

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Gaps

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0; Indels

Length 10461;

these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering

"these bases

/*tag= c

misc_feature

Treponema pallidum infection; syphilis; Borrelia infection; animal; ... enzyme production; ds.

Treponema pallidum

自然自然問題者是實際的名誉

X20553;

TESULT 94 120553

WO9859034-A2

/note;

(first entry)

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Rat nestin gene - its product is useful to identify brain tumours
                                                                 Q70447 standard; DNA; 11236 BP
                                                                                                                                                                                                           21-MAR-1995
                                                                                                                                      070447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a Kit for the immunodatection of saureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, oscenowielitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                           /note- "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
agreen in the specification for this DNA sequence"
7501..7560
                                                                                                                                                                                                                                                                                                                                              "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
given in the specification for this DNA sequence" 5701..5760
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in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18; Length 10813; 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived from stored on computer readable medium and used anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 17; DB
100.0%; Pred. No. 1.7
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1248-1254; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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/note= "thes
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Best Local Similarity 100
Matches 17; Conservative
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/note= "t
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                                                                 misc_feature
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070447 is the rat nestin gene encoding nestin protein (R60126).
Nestin protein expression distinguishes neural multipotential stem cells and brain tumour cells from the more differentiated neural. cell types (eg., neuronal, glial and muscle cells of the adult brian).
                                                              nestin gene; brain tumour; neoplastic cells; glial; neuronal; muscle; neural multipotential stem cell; mammalian brain; detection; diagnosis; medulloblastoma; gliablastoma; oligodendroglioma; ds.
                                                                                                                                                                                                                              'transl_except= pos:3087..3091, aa:His, Arg
'note= "sequence should be CAY CGG, ie. Y or C has
been deleted in the sequence given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain tumour
in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide and protein sequences for human and rat nestin distinguishes neural multipotential stem cells and brain tum cells from more differentiated cell types; for use in the
                                                                                                                                                                                                                                                                        /*tag= d
/note= "apparent inclusion of a nucleotide"
3375..4339
                                                                                                                                                     /*tag= a
/note= "start of primary transcript"
2589..10821
                                                                                                                                                                                              'product- Nestin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Column 25-34; 45pp; English.
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0180548.
88US-0201762.
90US-0603803.
91US-0660412.
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6120..6193
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6194..6388
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6389..10821
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4340..4464
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4465..61
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                                                                                                                                                                                                                                          /note=
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                                                                                                                                                                                                                                                             3104
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P-PSDB; R60126.
                                                                                                         Rattus rattus
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25-OCT-1990;
22-FEB-1991;
                                                                                                                               Key
misc_feature
                                                                                                                                                                                                          misc_feature
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Gaps

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Indels

Werner's syndrome; detection; diagnosis; autosomal; isorder; phenotype; ss.

recessive disorder; phenotype;

Mouse; WRN;

WO9724435-A1 Mus musculus

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Partial mouse WRN genomic sequence #1.

(first entry)

31-AUG-1999

x83005;

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                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
The nestin protein can be used in diagnosing tumours of the brain, such as medulloblastomas, gliablastomas and oligodendroglioma. (See also Q70448).
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                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide sequence from the genome of Treponema pallidum.
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                                                                                                                 Length 11236;
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                                                                    Sequence 11236 BP; 2876 A; 2678 C; 3258 G; 2424 T; 0 other
                                                                                                                                               Indels
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                                                                                                               Score 17; DB 15;
Pred. No. 1.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 389-401; 1150pp; English.
                                                                                                                                                                                                                                                                                    X20535 standard; DNA; 21170 BP.
                                                                                                               0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US13041.
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                                                                                                                                                                                                         3466 ccttcaggaagggctg 3482
                                                                                                               Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum
                                                                                                                                                                                                                                                                                                                                               05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9859034-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                  X20535;
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                                                                                                                                                                                                                                                                       :20535/c
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我的知意实现的最后就是不是不可以不知识的,我们就是不是不是不知识的。

Isolated nucleic acid molecule encoding the WRN gene product . useful for detection and treatment of Werner's syndrome, and related

ΰ Υū

Schellenberg GD,

Oshima J,

Mulligan J, WPI; 1997-363671/33

Fu Y,

MOLECULAR CORP

DARW-) DARWIN OSHI/) OSHIMA

96US-0594242

96US-0632175. 95US-0009409. 95US-0580539. 96US-0010835.

29-DEC-1995; 30-JAN-1996; 30-JAN-1996;

96WO-US20785

30-DEC-1996;

12-APR-1996 39-DEC-1995

10-JUL-1997

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This sequence represents a fragment of the genomic sequence containing the coding region for the mouse WRN gene (X83004). The corresponding human gene (X83001) encodes a protein related to Werner's syndrome. The products can be used for the detection and treatment of Werner's syndrome (WS), an autosomal recessive disorder with a complex phenotype,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subunit vaccine; nucleic acid immunisation; gene therapy; genetic disease; hemophilia; cystic fibrosis; cancer; viral infection; acquired immune deficiency syndrome; PAV antigen; porcine pathogen; ds.
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAV-3; defective recombinant PAV vector; live recombinant virus;
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                                                                                                                                                                                                                                                         Score 17; DB 18; Length 29604;
Pred. No. 1.6e+02;
                                                                                                                                                                                            Sequence 29604 BP; 7634 A; 5861 C; 5985 G; 10123 T; 1 other;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete nucleotide sequence of the PAV-3 genome
                                                                                                                                                                                                                                                                                                        Mismatches
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Claim 1; Fig 7; 153pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                Porcine adenovirus Type 3. .
                                                                                                                                                    as well as related diseases
                                                                                                                                                                                                                                                                                                                                                525 aaaggaatagaactggc 541
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The present sequence represents the complete nucleotide sequence of the genome of porcine adenovirus-3 (PAV-3). The specification also describes a defective recombinant PAV vector comprising inverted terminal repeats (ITR), packaging sequences and at least one heterologous nucleotide sequence (II), but lacking El functions. The defective vectors replicate inefficiently in cells (other than helper cells) so are unlikely to be immunogenic. Deletion of the El (and optionally other regions) increases the size of heterologous insert that can be packaged. The PAV-3 increases the size of heterologous insert that can be packaged. The PAV-3 increases polymucleotides sequences are used to produce (recombinant or defective) vectors that can express heterologous proteins, e.g. for making live, recombinant virus or subunit vaccines, for nucleic acid immunisation or for gene therapy (e.g. of genetic diseases such as hemophilia or cystic for gene therapy (e.g. of genetic diseases such as hemophilia or cystic deficiency syndrome), also for in vitro expression of recombinant antigens (for antibody production), antisense RNA, ribozymes or therapeutic proteins. They are also used diagnostically to detect PAV antigens and/or nucleic acid. The vectors may be used in human or vetering the proteins and proteins and proteins and proteins and proteins proteins and proteins 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      control expression of heterologous genes. Antibodies raised against PAV-3 polypeptides can also be used for diagnosis (to detect PAV-specific
New nucleic acids from the genome of porcine adenovirus-3, and derived gene therapy vectors, particularly for immunization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 veterinary medicine, but particularly for expressing protective determinants of porcine pathogens. Regulatory regions may be used to
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0/c Z32020 standard; DNA; 38734 BP. SESULT 100

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Human METH1 related EST AL021529. (first entry)

10-JAN-2000

Human; METH1; METH2; ant1-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; hebumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.

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They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders, ago be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. 232002 to 232080, and Y49503 to Y49511 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                    New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metalloprotease thrombospondin (METH) proteins METH1 and METH2 respectively. METH1 and METH2 have been found to be potent inhibitors angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemanglomas, and arterial-venous malformations.
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Match
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                                                                                                                                                                                                               nucleic
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Result No.

(1

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APPLICANT: Loosmore, Sheena M
APPLICANT: Loosmore, Sheena M
APPLICANT: Wang, Quijun
APPLICANT: Wang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FLING DATE: US/08/867,941
FILING DATE: 03-UN-1997
                                                                                                                                     Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PACENTIN RELEASE #1.0, VETSION #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/067,941
FILING DATE: 03-UON-1997
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Stewart, Michael 1
RECISTRATION NUMBER: 1038-681 MİS:jb
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3000 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 2;
Pred. No. 7.5;
0; Mismatches
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08867941 Patent No. 5977337 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             811 tcttggtgctcaaagcaaa 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 TCTTGGTGCTCAAAGCAAA 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6'
Best Local Similarity 100.'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
            TRY: Canada
M5G 1R7
Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-867-941-6
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                                                                                                                                                                                            APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quljun
APPLICANT: Yang, Yan-Ping
APPLICANT: Xled, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08867941
Patent No. 5977337
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: Du, Kun-Pan
APPLICANT: Wang, Quijun
APPLICANT: Wang, Yan-Ping
APPLICANT: Klein, Michal H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 2955; 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/867,941
FILING DATE: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                        E: Sim & McBurney
6th Floor, 330 University Avenue
                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19;
                                                                                                              Sequence 9, Application US/08867941 Patent No. 5977337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                       Loosmore, Sheena
Du, Run-Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LEMORY. ACC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 TCTTGGTGCTCAAAGCAAA 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                       STREET: 6th Floc
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
-S-08-867-941-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 2
5-08-867-941-8
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(416) 595-1155

5: Sim & McBurney 6th Floor, 330 University Avenue

CORRESPONDENCE ADDRESS

ADDRESSEE:

STREET: bun

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Gaps

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Length 3000; 0; Indels

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Sequence 3, Application US/09045186
Patent No. 6087154
GENERAL INPORMATION:
APPLICANT: Baez, Melvyn
APPLICANT: Cates, Carolyn A.
TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
                                                                                                                                                                                   STATE: Indiana COUNTRY: United States of America 21P. 46285
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                STREET: Lill Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (317) 276-3861 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                 Length 7641;
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                                                                                                                                                                                       0; Indels
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APPLICANT: Bacz, Melvyn
APPLICANT: Cates, Carollyn A.

TITLE OF INVENTION: RHESUS NEUROPEPTIDE YI RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company
STREET: Lill Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America
21P: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
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red. No. 23;
Mismatches 0
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Pred. No.
                                                                                                                                      0.6%; Scu.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGERATION UNDRER: 36,808
REFERENCE/POCKET NUMBER: P-11:
TELECOMMUNICATION INFORMATION:
TELEPANE: (317) 276-0756
TELEPANE: (317) 276-0756
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09045186 Patent No. 6087154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pr
                                                                                                                                                                                                                     2802 aaagaagtcttggaaaca 2819
     SEQUENCE CHARACTERISTICS:
LENGTH: 7641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1152 base pairs
                                                                                                                                               Query Match 0.61
Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 100.'
Matches 18; Conservative
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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13-09-045-186-1
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S-09-045-186-1/c
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(317) 276-0756

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Length 1152;
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHIBANO, YUJI
APPLICANT: KIKUCHI, NORIHISA
APPLICANT: ODA, KOHEI
TITLE OF INVENTION: NOVEL PROTEINASE INHIBITOR FITTLE OF INVENTION: GENE ENCODING THE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RASKIN & DAVIDSON P.C.
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1140 AVENUE OF THE AMERICAS CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: 'Floppy disk
IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
                                                                                                                                                        0.0°,
100.0%; Pr
                                                                                                                                                                                                                                                                                                                     RESULT 6
US-08-878-546-9
; Sequence 9, Application US/08878546
; Patent No. 5952463
                                                                                                                                                                                                                                                  2802 aaagaagtcttggaaaca 2819
                                                                                                                                                          Query Match 0.6
Best Local Similarity 100.
Matches 18; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
                                 nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPÜTER READABLE FORM: MEDIUM TYPE: 'Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEINBERG
                                                                                 , MOLECULE TYPE: mRNA
US-09-045-186-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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1091 AAAGAAGTCTTGGAAACA 1074

*ESULT 5 ::S-09-045-186-3/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: /note= "cDNA clone cc43 of 4 kb; OTHER INFORMATION: transcript"
US-08-680-395-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ore 18; DB 2;
red. No. 23;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PRO'
TITLE OF INVENTION: 10 ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESSE:
ADDRESSET: High Street Tower' - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18;
APPLICATION NUMBER: US/08/680,395
FILING DATE: 15-JUL-1996
CLESSIFICATION: 435
ALTORNEY/AGENT INFORMATION:
NAME: Bastlan, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-967-101-23/c
; Sequence 23, Application US/08967101
; Patent No. 5840540
                                                                                              NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFRENCE/DOCKET NUMBER: 02307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENTE: 2605 base pairs
TEMPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1421 TTCCAAAGTGTGTACTTT 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 ttccaaagtgtgtacttt 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: - LOCATION: 1..2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08680395
Sequence 4, Application US/08680395
Sequence 4, Application US/08680395
Sequence 4, Application US/08680395
Sequence 4, Application US/08680395
Sequence 4, Application Gray, Joe W.
APPLICANT: Gray, Joe W.
APPLICANT: Godfrey, Tony
APPLICANT: Rommens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 18; DB 2; Length 2186; 100.0%; Pred. No. 23; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 158677/1996
FILING DATE: 19-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 24104/1996
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 48101/1997
FILING DATE: 03-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: DAVIDSON, CLIFFORD M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 32,728
REFERENCE/CAST NUMBER: 32,728
REFERENCE/CENT NUMBER: 32,728
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

ANDIUM TYPE: Floppy disk
  APPLICATION NUMBER: US/08/878,546 FILING DATE: 19-JUN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: STREPTOMYCES PLATENSIS STRAIN: Q268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1518 GGTCCTGGGCACCCTGGC 1535
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Best Local Similarity 100.0
Matches 18; Conservative
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LOCATION: 1477..1911
.3-08-878-546-9
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NAMI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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APPLICANT: Rim, Jungsuh P.
APPLICANT: Reyes, Gregory R.
APPLICANT: Wages, John
APPLICANT: Young, LaVonne
APPLICANT: Young, LaVonne
ATILE OF INVENTION: No. 5859230-A/No. 5859230-B/No. 5859230-C/No. 5859230-D/No.
GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
183
                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
                                                                                               HURWITZ & THIBEAULT
et Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 17;
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/124,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08611757; Patent No. 5895230 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Kim, Jungsuh P.
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
US-09-124-698-23
                                                                                                                  High Street Tower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                     Massachusetts
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CORRESPONDENCE ADDRESS:
                                                            NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HU
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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Matches 17; Conserve
                             FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                     U.S.A.
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                                                                                                                                      Boston
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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US-08-611-757-20/c
                                                                                                                                                                     COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE
                                                                                                                   STREET:
              APPLICANT:
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                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 289;
                                                                                                                   Length 289;
                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: Datentin Release #1.0, Version #1.30 CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/592,541 FILING DATE: CLASSIFICATION: 800 ATTONEX/AGENT THING ATTONEX/AGENT THING ATTONEX/AGENT THING ATTONEX/AGENT THING
                                                                                                                  DB 2;
71;
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71;
                                                                                                                                                     Mismatches
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Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
                                                                                                                   Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17;
                                                                                                     0.6%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: PICCHE, EGMUNG R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.6%; So
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2131 aagaggaagcagtggaa 2147
                                                                                                                                                                                      2131 aagaggaagcagtggaa 2147
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                                                                                                                                                                                                                       267 AAGAGGAAGCAGTGGAA 251
                                                                                                                Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 289 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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              STRANDEDNESS:
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                                                                                                                                                                                                                                                                            ESULT 9
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Gaps

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Length 289; Indels

DB 3; 71;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 2
Pred. No. 72;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  ANTI-SENSE: NO
CONGINEL SOURCE:
INDIVIDUAL ISOLATE: NY 190 Clone D30
PCT-US95-05980-20
                                                                                                                                                                                                                                                                                                                                   Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curtis, Morris & Safford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 110, Application US/08184009 Patent No. 5833975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
0;
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINAL
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION
                TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 304 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                  132 cgccgcgagcggccgcg 148
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                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-A/Non-B/Non-C/Non-D/Non-E Hepatitis
Agents and Molecular Cloning Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: My 190 Clone D30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17;
Pred. No.
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,985
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: 05.396
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/922,493
FILING DATE: 30-UL1-192
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/246,986
APPLING DATE: 20-MAX-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
RESIGNEATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0201.4
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4600-0201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/611,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TT-US95-05980-20/c
Sequence 20, Application PC/TUS9505980
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 cgccgcgagcggccgcg 148
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 304 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 CGCCGCGAGCGGCCGCG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NO TITLE OF INVENTION: AG NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 350 Camt
CITY: Palo Alto
STATE: CA
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MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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APPLICANT:
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Mismatches
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ATTONNEY FAGENT UNFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 840-3133
TELEX: (212) 840-0712
TELEX: (220) 840-0712
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
3: Curtis, Morris & Safford
530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           томыек: US/08/184,009
19-JAN-1994
N: '.
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APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 109, Application US/08458356 Patent No. 5942235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 GGTCCTGGGCACCCTGG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1094 base pairs
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APPLICATION NUMBER: US,
FILING DATE: 19-JAN-195
CLASSIFICATION: 435
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EDNESS: single
                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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CLASSIFICATION:
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                                          New York
                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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  ADDRESSEE:
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                                                                                COUNTRY:
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Patent No. 5833975
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tarteglia, James
APPLICANT: Tarteglia, James
APPLICANT: Tarteglia, Is TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
RERENCE/DOCKET NUMBER: 454310-2530
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                             E: Curtis, Morris & Safford
530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                       Sequence 110 ; Sequence 110, Application US/08458356; Patent No. 5942235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 42506GURMS
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1652 ggtcctgggcaccctgg 1668
                   1652 ggtcctgggcacctgg 1668
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                                                           292 GGTCCTGGGCACCCTGG 308
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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Gaps
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APPLICANT: Tartaglia, James
APPLICANT: Tox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
CORRESPONDENCE ADDRESS: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
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GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie;
APPLICANT: DE SMET. Charles;
APPLICANT: BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,528C
FILING DATE: April 25, 1997
CLASSIFICATION: 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: CELL DIVISION REGULATORS
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17;
                                                                                                                                                                                                         Sequence 8, Application US/08845528C Patent No. 6027924
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Bandman, Olga
Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08951148
; Patent No. 5871973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.6%; So
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
  Best Local Similarity 100.0%; F
Matches 17; Conservative 0;
                                                              1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1652 ggtcctgggcaccctgg 1668
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 GGTCCTGGGCACCCTGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York City
: New York
RY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New YOUNGE: New YOUNTRY: US
                                                                                                                                                                                       US-08-845-528C-8
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US-08-951-148-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LUCAS, Sophie;
APPLICANT: DE SMET, Charles;
APPLICANT: BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & T...
STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1691;
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                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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APPLICATION NUMBER: US/08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MATY Anne Schofleld
REGISTRATION NUMBER: 36,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08993118 Patent No. 5997872
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 4543
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
TELEFAX: (212) 840-0712
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1094 base pairs
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                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ET: 805 Third Avenue
: New York City
E: New York
FRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        1652 ggtcctgggcacctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 GGTCCTGGGCACCCTGG 330
                                                                                                                                                                                                                                                                                                                               Ouery Match 0.64
Best Local Similarity 1000
Matches 17; Conservative
                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotides
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                                                                                                                                                                                                                                TOPOLOGY: 1i
MOLECULE TYPE:
75-08-458-356-109
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Gaps
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APPLICANT: Bandman, Olga
APPLICANT: Lal, Preett
APPLICANT: Shin, Purett
APPLICANT: Shin, Purvi
APPLICANT: Shin, Purvi
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/274,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/951,148
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/951,148
                                                                    APPLICATED STEEN TO THE ORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-O
TELECOMMUNICATION INFORMATION:
THE TENDENCE STEEN ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Scc.
100.0%; Prr
0;
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"ATTORNET/AGENT INFORMATION:
NAME: BILLLINGS, LUCY J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEGUENCE CHARACTERISTICS:
LENGTH: 1816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  804 ggaaacttcttggtgct 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       717 GGAAACTICTIGGIGCT 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
TELEX:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linea; IMMEDIATE SOURCE: LIERARY: SPLNFZ; CLONE: 26459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
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STREET: 31
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US-09-274-570-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Durvi
TITLE CP INVENTION: CELL DIVISION REGULATORS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastERD for Windows Version 2.0
CHRENT APPLICATION DARE: US/09/165,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
              Incyte Pharmaceuticals, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17;
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09165234 Patent No. 5928899
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Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
ADDRESSEE: Incyle ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     717 GGAAACTTCTTGGTGCT 733
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                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
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                               STREET: 31/7.
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TOPOLOGY: LILL
IMMEDIATE SOURCE:
LIBRARY: SPENE?
TOWE: 26459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                         USA
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ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA
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                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: .:
.:S-08-951-148-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-09-165-234-2
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S S

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GENERAL INFORMATION:
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 17; DB 1; Length 2419;
100.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DALL.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
APPLICATION NUMBER: 26-MARCH-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                   Sequence 7, Application US/08299849B Patent No. 5612201
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                                                                                                                                                                                                                                                                                                                                                                                SSSEE: Felfe & Lynch
TT: 805 Third Avenue
New York City
New York
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: genomic DNA
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                                          739 GGTCCTGGGCACCCTGG 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches, 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/07807043B
Patent No. 5342774
GENERAL INFORMATION:
APPLICARW: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Refection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 17; DB 1; Length 2419;
100.0%; Pred. No. 73;
                                                                                                                                                                                                                     Length 1816;
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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tive 0; Mismatches
                                                                                                                                                                                                                                                                         Mismatches
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10D 253.3
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-984
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION DATE: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,138
FILING DATE: 3-MAY-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                   804 ggaaacttcttggtgct 820
                                                                                                                                                                                                                                                                                                                                          717 GGAAACTTCTTGGTGCT 733
                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                           LIBRARY: SPLNFZT01
CLONE: 26459
.3-09-274-570-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
LENGIH:
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APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                   STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLICASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 90,037,230
FILING DATE: 22-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/80,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 6025474man D.
REGISTRATION NUMBER: 30,946
RECISTRATION NUMBER: 20,946
REFERNICE/DOCKET NUMBER: 20,946
RECISTRATION NUMBER: 20,946
REFERENICE/DOCKET NUMBER: 20,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/967,727
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; Sequence 23, Application US/08465167A
; Patent No., 5750395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08; Pr.
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APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Stdney, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.68;
                                                                                                                                                                            ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: genomic DNA US-08-967-727-7
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                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
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Best Local Similarity 100.
Matches 17; Conservative
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van Gen Falleur, Thierry; Van der Bruggen, Thierry;
APPLICANT: Van den Eynde, Bener, Van Rel, Aline; De Planen, Etienne;
APPLICANT: Uurquin, Christophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
CITY: New York
CITY: New York
STATE: New York
STATE: New York
STATE: Diskette, 5.25 inch, 360 kb storage
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Mismatches
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PRICR APPLICATION: 435

PRICR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354

FILING DATE: 22-MAY 1992

PRICR APPLICATION UNBER: 07/807,043

FILING DATE: 12-DECEMBER-1991

PRICR APPLICATION UNBER: 07/764,364

FILING DATE: 23-SEPTEMBER-1991

PRICR APPLICATION UNBER: 9-JULY-1991

PRICR APPLICATION NUMBER: 9-JULY-1991

PRICR APPLICATION NUMBER: 9-JULY-1991

PRICR APPLICATION NUMBER: 9-JULY-1991

PRICR APPLICATION NUMBER: 9-JULY-1991

RELING DATE: 23-MAY-1991

APPLICATION NUMBER: 9-JULY-1991

APPLICATION NUMBER: 9-JULY-1991

APPLICATION NUMBER: 21-MAY-1991

APPLICATION NUMBER: 21-MAY-1991

ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 5925729man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 52
TELECOMUNICATION INPORMATION:
                                                                                                  Sequence 7, Application US/08142368A
Patent No. 5925729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Scilarity 100.0%; P. Conservative 0;
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1652 ggtcctgggcaccctgg 1668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               739 GGTCCTGGGCACCCTGG 755
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :S-08-142-368A-7
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US-08-967-727-7
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Sequence 7, Application US/08967727 Patent No. 6025474

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Nicotiana tabacum
N. tabacum cv. Xanthi
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100.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1. Application US/08343760A; Patent No. 5679783; GENERAL INFORMATION: The PAPLICANT: De Robertis, Edward M APPLICANT: De Robertis, Edward M APPLICANT: Sasal, Yoshiki; TITLE OF INVENTION: Tissue Differentiation Affecting; TITLE OF INVENTION: Factor and Composition NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSE: Majestic, Parsons, Siebert & Hsue STREET: Four Embarcadero Center, Suite 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,760A
FILING DATE: 22-NOV-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from 1 to 143 bp: Leader
non translated 5 sequence (leader)
from 144 to 2855 bp: coding sequence
for nitrate reductase apoenzyme
from 2856 to 3457 bp: non translated
3 sequence
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                                                                                   PCI/FR 93/00222
                                                                                                                                                                                                                                                                                               LENGIH: 3457 base pairs
TYPE: nucleotide with corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
CELL LINE:
                      US/08/295,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93
FILING DATE: March 5, 1993
APPLICATION NUMBER: 92 02658
FILING DATE: March 5, 1992
ATTORNEY/AGENT INFORMATION:
NAME: PROUL, D. BRUCE
REGISTRATION NUMBER: 20,958
REFERENCE/POCKET NUMBER: 2720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nitrate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                (1.vi.A)
(1.vi.B)
XHFD 8
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Best Local Similarity 100.
Matches 17; Conservative
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                               single
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
STRANDEDNESS:
TOPOLOGY: linea
MOLECULE TYPE: CD
ORIGINAL SOURCE:
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ORIGINAL SOURCE:
ORIGINAL SOURCE:
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LOCATION:
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LOCATION:
LOCATION:
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STATE: C
COUNTRY:
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Pred. No. 73;
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TITLE OF INVENTION: DNA ENCODING MAGE-I C-TERMINAL TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended) CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               MEDIUM TYPE: FLOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CORFRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATENTE 05-AUG-1993
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 11,990
                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CIII: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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STREET: P.O. Box 7068
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08295882 Patent No. 5569833 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatib]
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TITLE OF INVENTION: PLAN
TITLE OF INVENTION: STOR
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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ZIP: 91109-7068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626..1552
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SOFTWARE: WORD PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
US-08-465-167A-23
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Gaps
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APPLICANT: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors,
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                      CHROMOSOME/SEGMENT: (of corresponding genomic gene)
CHROMOSOME/SEGMENT: 9q
MAP POSITION: 22.3
MAP THE CONTRACTOR OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIII.
CITIE. New York
ZIP: 1002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ore 17; DB 1;
Pred. No. 73;
Mismatches 0
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CLASSIFICATION 1424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702

FILING DATE: 23-May-1991

ATTONNEY, AGENT INFORMATION:
NAME: HANSON, NO. 5342774man D.
REGISTRATION NUMBER: 30,946

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: 10D 253.3

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/07807043B Patent No. 5342774
       CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4189 IGAAGCCACCTGGAAG 4205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2105 tgaagccaccctggaag 2121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5674 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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STRANDEDNESS: singular
                                                                                                                                     ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: Human cDNA
POSITION IN GENOME: (of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: MAGE-1 gene
US-07-807-043B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 805 THE CITY New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linear
                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-07-807-043B-8
                                                                                                                                                                                                                                                                                                                                                                               US-08-441-430-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Buthwald, Manuel
APPLICANT: Strathdee, Craig A.
APPLICANT: Wevrick, Rachel
APPLICANT: Wevrick, Rachel
APPLICANT: Wevrick, Rachel
APPLICANT: Wethew, Christopher George Porter
TITLE OF INVENTION: Fanconi Anemia Type C Gene
NUMBER OF ENGUENCES: 73
CORRESPONDENCE Richard J. Polley, Esq.
ADDRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Richard J. Polley, Sq.
ADDRESSEE: Richard J. Salmon, Suite 1600
CITY: Portland
STREET: 121 S.W. Salmon, Suite 1600
COMPUTEY: U.S.A.
ZIP: 97204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMUTER READABLE FORM:
MEDIUM TYPE: Disk, 34-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1/ASCII Text File
CURRENT APPLICATION DATA:
APPLICATION NATA:
TELING DATE: MAY 15, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: April 29, 1992
APPLICATION NUMBER: U.S. 07/918,313
FILING DATE: July 21, 1992
APPLICATION NUMBER: U.S. 08/003,963
FILING DATE: JANUARY 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley, ESG.
REGISTATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 3812-42824
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 28,758
REPERRUCE/DOCKET NUMBER: 3100.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 362-556
TELERAX: (415) 362-5418
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3796 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Nucleic Acid
STRANDEDNESS: Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4488 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1036 CTCTACGTCTTCTCCGA 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 ctctacgtcttctccga 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.1
Matches 17; Conservative
                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                            . MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08299849B
Patent No. 5612201
GENERAL INFORMATION:
APPLICANT: De Jean, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
                                                                                                                                                                                                   ö
                                                                                                                0.6%; Score 17; DB 1; Length 5674;
100.0%; Pred. No. 73;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IEM
COMPUTER: IEM
COMPUTER: IEM
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTONNEY AGENT INFORMATION:
REGISTRATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTONNEY AGENT INFORMATION:
REGISTRATION NUMBER: 30,946
REFERENCE-DOCKET NUMBER: 10,946
REFERENCE-DOCKET NUMBER: 10,946
REFERENCE-DOCKET NUMBER: 10,946
REFERENCE-DOCKET NUMBER: 10,946
REFERENCE-DOCKET NUMBER: 30,946
REFER
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LLE: Felfe & Lynch
KRET: 805 Third Avenue
TY: New York City
TE: New York
TOO22
                                                                                                                                                                                                                                                                                                                                   3994 GGTCCTGGGCACCCTGG 4010
                                                                                                                                                                                                                                                                                  1652 ggtcctgggcacctgg 1668
                                                                                                                Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: MAGE-1 gene
US-08-299-849B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 80
US-08-190-411A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence 1, Application US/08190411A

Sequence 1, Application US/08190411A

Sequence 1, Application US/08190411A

Sequence 1, Application US/08190411A

RAPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
APPLICANT: Old, Lloyd Selection Plerre; Boon-Falleur, Thierry;
APPLICANT: Old, Lloyd J

TITLE OF INVENTION: WONOCLONAL ANTIBODIES WHICE IN THE OF INVENTION: TUMOR REJECTION ANTICEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1, TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES

NUMBER OF SEQUENCES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue

CITY: New York City
                                                                                                                                                             Gaps
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                                                 ore 17; DB 1; Length 5674;
red. No. 73;
Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
TOTAL TYPE: DISKETTE, 5.25 inch, 360 kb storage
TOTAL TYPE: DISKETTE, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,411A
FILING DATE: 01-FEBRUARY-1994
CLASSIFICATION: 436
PRIOR APPLICATION 136
PRIOR APPLICATION ON THE CONTROL OF THE CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, No. 5541104man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 53:
                                                                                   100.0%; Pre
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          3994 GGTCCTGGGCACCCTGG 4010
                                                                                                                                                                                                                                            1652 ggtcctgggcaccctgg 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                          Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MAGE-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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GENERAL INFORMATION:
APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
APPLICANT: Lurquin, Chistophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSED:
ADDRESSED: Felfe & Lynch
                                                                                                                                                                 Gaps
                                                                                                                                                              ö
                                                                                                        Length 5674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                      DB 2;
73;
                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/64,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
ATTORNEY/AGENT INFORMATION:
NAME: YAGORATON NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: YAGORATON NUMBER: 07/705,702
NAME: YAGORATON NUMBER: 07/705,702
                                                                                                           Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson, No. 5925729man D.
                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/08142368A; Patent No. 5925729
                                                                                                   Query Match 0.6%; Sc
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 1652 ggtcctgggcacctgg 1668
                                                                                                                                                                                                                                                                       3994 GGTCCTGGGCACCCTGG 4010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5674 base pairs
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MAGE-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York City
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIT:.
STATE: Ne.
10022
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US-08-560-024-1
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                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08560024

Patent No. 5843448

GENERAL INFORMATION:
APPLICANT: Chen, Yac-Tseng; Stockert, Elisabeth;
APPLICANT: Chen, Yachi, Garin-Chesa, Pilar; Rettig, Wolfgang J.;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES

TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
                                                                                  Gaps
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                         DB 1; Length 5674; 73;
                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:

CORRESPONDENCES:

ADDRESSE: Felfe & Lynch
STREET: New York City
STAFE: New York
ZIP: 1002-Z
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S/08/190,411
FILING DATE: 01-FEBRUAR-1994
APPLICATION NUMBER: 037,230
FILOR DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 9-JULY-1991
APPLICATION NUMBER: 9-JULY-1991
ATPORNEY/AGENT NUNDER: 07/705,702
FILING DATE: 23-MAY-1991
ATPORNEY/AGENT NUNDERS: 07/705,702
FILING DATE: 13-MAY-1991
ATPORNEY/AGENT NUNDERS: 07/705,702
FILING DATE: 13-MAY-1991
ATPORNEY/AGENT NUNDERS: 07/705,702
                      ch 0.6%; Score 17; 1 Similarity 100.0%; Pred. No. 17; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, NO. 5843448man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5354
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TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                     1652 ggtcctgggcacctgg 1668
                                                                                                                                                                                        3994 GGTCCTGGGCACCCTGG 4010
                                                     Best Local Similarity
Matches 17; Conserv
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                            Query Match
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Gaps
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                                                                                                                                                                                                                                                           APPLICANT: DEGOCHI, Takeo
APPLICANT: ENOSHITA, Moritoshi
APPLICANT: KINOSHITA, Moritoshi
APPLICANT: KATSURAGI, Kiyonori
APPLICANT: SHIN, Sadahito
TITLE OF INVENTION: HUMAN ARYLAMINE N-ACETYLITRANSFERASE
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughtue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6464;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,478
FILING DATE: 11-0CT-1994
CLASSIFICATION: 435
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/038,667
FILING DATE: 23-MAR-1993
APPLICATION NUMBER: TP 64669/1992
FILING DATE: 23-MAR-1992
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 293-7660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States
ZIP: 20037-3202
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   US-08-321-478-6

'Sequence 6, Application US/08321478

· Patent No. 5527677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Querý Match 0.6%; Sc
Besť Local Similarity 100.0%; P
Matches 17; Conservative 0;
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                           1652 ggtcctgggcacctgg 1668
                                                                                     3994 GGTCCTGGGCACCCTGG 4010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1032 aggtaccaaggaaaggc 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5916 AGGTACCAAGGAAAGGC 5932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyA_signal
1794..1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_signal
1800..1805
17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    723..1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-08-321-478-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
Matches
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;

APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;

APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For

TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

UNDBER OF SEQUENCES:

ADDRESSEE: Felfe Lynch

STRET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                  ö
                                                                Gaps
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                Length 5674;
                                                                0; Indels
                    DB 2;
73;
                  Score 17; DB 2
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION 1435

PRIOR APPLICATION NUMBER: 08/037,230

FILING DATE: 26-WARCH-1993

APPLICATION NUMBER: PCT/US92/04354

FILING DATE: 12-DECEMBER-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/84,365

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365

FILING DATE: 3-SEPTEMBER-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838

FILING DATE: 23-MAY-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702

FILING DATE: 12-MAY-1991

PRIOR APPLICATION NUMBER: 07/705,702

FILING DATE: 12-MAY-1991

ATTORNEY/AGENT INFORMATION:
NUMBER: 07/705,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 17;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hanson, No. 6025474man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
                                                                                                                                                                                                                                                                Sequence 8, Application US/08967727
Patent No. 6025474
                  Query Match 0.6%; Some Best Local Similarity 100.0%; P. Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO. 8
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                            MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MAGE-1 gene
3-08-967-727-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Length 29604;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
TITLE OF INVENTION, GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,891

FILING DATE: 27-DEC-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: NO. 6090620tenburg Ph.D., Carol

REGISTRATION NUMBER: 39,317

REFERENCE/DOCKET NUMBER: 240052.419

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-6031

INFORMATION FOR SEQ ID NO: 207:

SEQUENCE CHARACTERISTICS:
                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 3;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 17; DB 3; Best Local Similarity 100.0%; Pred. No. 75; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFWARE: PATENTIN VET. 2.0
SEQ ID NO 1
                                                                                                                                                             STREET: 6300 Columbia Center, 701
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILIBLE
COMPUTER: IBM PC COMPAILIBLE
COMPUTER: PARTEN: PC-DOS/MS-DOS/SOFTWARE: PATENTIN Release #1.0, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 39
US-09-335-409-1/c
; Sequence 1, Application US/09335409
; Patent No. 6121029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Sorangium cellulosum
US-09-335-409-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 14826 AAAGGAATAGAACTGGC 14842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 29604 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                525 aaaggaatagaactggc'541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.6
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-781-891-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 68750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
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                                                                                                                                                           APPLICANT: McKay, Ronald D.G.
APPLICANT: Lendahl, Urban
TITLE OF INVENTION: Nestin Expression As An Indicator of
TITLE OF INVENTION: Neuroepithelial Tumors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/853,913

FILING DATE: 19920319

FILING DATE: 22-FEB-1991

PRIOR APPLICATION NUMBER: US 07/660,412

FILING DATE: 22-FEB-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,803

FILING DATE: 25-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/201,762

FILING DATE: 02-JUN-1988

FILING DATE: 02-JUN-1988

FILING DATE: 02-JUN-1988

PRIOR APPLICATION DATE: US 07/201,762

REPERENCE/OCKET INFORMATION:

NAME: GRADAIN NUMBER: US 07/180,548

ATTORNEY/AGRAT INFORMATION:

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-4641AAAA

TELEFRAN: 617-861-6340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-08-781-891-207
Sequence 207, Application US/08781891
Setent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
                                                                                        Sequence 1, Application US/07853913
Patent No. 5338839
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .y 1877 ccttcaggaagggctg 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3466 CCTTCAGGAAGGGGCTG 3482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11236 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
                                                                                                                                                                                                                                                                                                                                                           CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-07-853-913-1
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Gaps

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TITLE OF INVENTION: METHOD FOR SYNTHESIZING STABLE
TITLE OF INVENTION: SINGLE-STRANDED CONA IN EUKARYOTES BY MEANS OF A BACTERIAL
TITLE OF INVENTION: RETRON, PRODUCTS AND USES THEREFOR
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/503,730
FILING DATE: 18-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Weiser & Associates
230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 16; DB 1; 387.5%; Pred. No. 2.2e+02; Live 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Welser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377(913).6277P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
                                                                                        APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: NEW HYBRID MOLECULES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMERS: US 07/817,430
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   Sequence 16, Application US/08503730 Patent No. 5780269 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/08507634 Patent No. 5849563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Miyata, Shohei
APPLICANT: Onshima, Atsushi
APPLICANT: Inouye, Suniko
APPLICANT: Inouye, Masayori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2165 gtcccaagccatcagc 2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser &
STREET: 230 South Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                           RY: USA
19102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                     STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 42
US-08-507-634-13
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JS-08-503-730-16
                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                 APPLICANT: Miyata, Shohel
APPLICANT: Obshima, Atsushi
APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: METHOD FOR SYNTHESIZING STABLE
TITLE OF INVENTION: SINGLE-STRANDED CDNA IN EURARYOTES BY MEANS OF A BACTERIAL
TITLE OF INVENTION: RETRON, PRODUCTS AND USES THEREFOR
NUMBER OF SEQUENCES: 20
OCRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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bond to nucleotides 156-163 of SEQ ID NO: 11 of
this application."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/753,110B
FILLNG DATE: 30-AUG-1991
CLASSIFICATION: 435
                                                                                                                                                             Sequence 12, Application US/07753110B Patent No. 5436141 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
RECISTRATION UNBERE: 19,763
REFERENCE/DOCKET NUMBER: 377.5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                              20332 ceeccaecccaecae 20316
  1457 cggcccagccccagcag 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2165 gtcccaagccatcagc 2180
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LOCATION: 69.76
OTHER INFORMATION: COTHER INFORMATION: bond
OTHER INFORMATION: this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 87.5 Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                              38-07-753-110B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Human RAD50 Gene and Methods of Use Thereof 175
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSITCATION: 435
PRIOR APPLICATION UMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTONINEY/AGENT INFORMATION:
ANAMERICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTONINEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16; DB 3; 1
Pred. No. 2.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 70, Application US/08687080
Fatent No. 5965427
GENERAL INFORMATION:
TITLE OF INVENTION: Human RAD50 Gene and Metical Correspondence Addresses: 175
CORRESPONDENCES: 175
ADDRESSES: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                      00786/345001
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.5%; Sco
Best Local Similarity 100.0%; P:
Matches 16; Conservative 0;
                                                     ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sholtz, Charles K. REISTRAITON NUMBER: 38 615 REFERENCE/DOCKET NUMBER: 46 TELECOMMUNICATION INFORMATION:
                                                                                                                  REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101 gacagcaggtaccagc 1116
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 233 base pairs
nuclëic acid
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COMPUTER READABLE FORM:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE:
US-08-717-294-93
                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 44
US-08-687-080-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide is linked to the 5' position of nucleotide number 1 of SEQ ID NO: 12 of this application."
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bond to nucleotides 156-163 of Si
this application."
                                                                      CORTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,634
FILING DATE: 25-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.6282P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-875-838
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 16; DB 2; 87.5%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SEED, BRIAN
APPLICANT: HAAS, JURGEN
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESSE:
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 93, Application US/08717294 Patent No. 6114148 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 19
COCHER INFORMATION: note-
OTHER INFORMATION: nucleor other Information: applic praylure: name of the nucleor other information: applic praylure: name of the nucleor other information: note-
OTHER INFORMATION: hote-
OTHER INFORMATION: hote-
SS-08-507-634-13
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2165 gtcccaagccatcagc 2180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 176 Fe
CITY: Boston
STATE: MA
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APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Gaines, Partick J.
APPLICANT: Gaines, Partick J.
APPLICANT: Sluver, Gary
APPLICANT: Sluver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
AUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
ADDRESSEE: Sheridan Ross & McIntosh
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
WUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/005,069 FILING DATE:
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100.0%; Pred. No. 2.2
ive 0; Mismatches
                                                                                                                                                    ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,822
ATTORNEY AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-023
INFORMATION FOR EQU ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104, Application US/08906769 Patent No. 6077687 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1478 aagaagtcagtaccca 1493
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                    CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-906-769-104/c
                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us-09-002-069-97
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                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNDER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
                                                                                                                              Score 16; DB 2; Length 233;
Pred. No. 2.2e+02;
            ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: INTRON 6 OF RAD50 GENOMIC SEQUENCE:3-08-687-080-70
                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: COLORAdo
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2e+02;
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                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/630,822A
FILING DATE: 11-APR-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                     S-08-630-822A-97/c
Sequence 97, Application US/08630822A
Patent No. 5840695
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Sequence 97, Application US/09005069
Patent No. 5932470
EBENEAL INFORMATION:
APPLICANT: FRANK, GLENN R.
                                                                                                                              Query Match 0.5%; Sco
Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-6223
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (y 1478 aagaagtcagtaccca 1493
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                966 tttgtggtggtagaat 981
                                                                                                                                                                                                                                                                         2 TTTGTGGTGGTAGAAT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
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Length 252;

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                 /note= "At pos. bp 4, change A to
R. At pos. aa 2, substitute Xaa."
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SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16; DB 3; Lv
Pred. No. 2.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULES, AND USES THEREOF
          NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104, Application US/08817795
Patent No. 6139840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rank, Glenn R.
Heath, Andrew W.
Tamaka, Miles Yamanaka
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Dale, Beverly
Stiegler, Gary
NVENTION: USE OF PRO'
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NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grieve, Robert B.
Rushlow, Keith E.
Hunter, Shirley Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1478 aagaagtcagtaccca 1493
                                                                                                                                                                                        LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: , OTHER INFORMATION: R US-08-906-616-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDACTOR TO STREET: 1/2.
CITY: Denver STATE: Colorado
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
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APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Silver, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 0.5%; Score 16; DB 3; Length 252; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "At pos. bp 4, change A to R. At pos. aa 2, substitute Xaa."
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
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                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/906,616
05-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 104, Application US/08906616
Patent No. 6121035
GENERAL INFORMATION:
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ADDRESSEE: Sheridan Ross P.C.
COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/Men-BOUTHARE: Patonia
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 104
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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OTHER INFORMATION:
OTHER INFORMATION:
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STATE: Colorado
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :S-08-906-616-104/c
                                                                                                                                                     FILING DATE
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FLEA PROTEASE PROTEINS,
                                                                                                                  Length 252;
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                                /note= "At pos. bp 4, change A to R. At pos. aa 2, substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stiegler, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT R
TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCI/US95/14442A
                                                                                                                  DB 3; L
                                                                                                                  0.5%; Score 16; DB 100.0%; Pred. No. 2.2 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                   Sequence 104, Application PC/TUS9514442A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Grieve, Robert B.
Rushlow, Keith E.
Hunrer, Shirley Wu
Frank, Glenn R.
Heath, Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (303) 865-9700
TELEFAX: (303 863-0223
INFORMATION FOR SEQ ID NO: 104
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      1478 aagaagtcagtaccca 1493
                                                                                                                  Query Match 0.5%
Best Local Similarity 100.0
Matches 16; Conservative
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                 LOCATION: 1..251
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colorado
: USA
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                                                                   US-08-639-075A-104
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ZIP: 80203
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                                                                                                                                                                                                                                                                                                          Length 252;
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100.0%; Pred. No. 2.2e+02;
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RPPLICANT: Stiegler, Gary
RPPLICANT: Gaines, Patrick J.
RPPLICANT: Silver, Gary
RPLICE OF INVENTION: FLEA PROTEASE PROTEINS, NU
FILLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                           Mismatches
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STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104, Application US/08639075A Patent No. 6150125 GENERAL INFORMATION: APPLICANT: Grieve, Robert B.
                                                                                                                                                                                                                        NAME/KEY: Xaa - any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grieve, Robert B.
Rushlow, Keith E.
Wu Hunter, Shirley
Frank, Glenn R.
TELEPHONE: (303) 863-9700
TELEFAX: (303 863-0223
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      1478 aagaagtcagtaccca 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 252 base pairs
nucleic acid
EDNESS: single
                                                                       : 252 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                         199 AAGAAGTCAGTACCCA 184
                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                linear
                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1..251
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-08-639-075A-104/c
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                                                                                                                                                                                                                                      LOCATION:
"5-08-817-795-104
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APPLICANT:
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APPLICANT:
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KUZ: A No. 5935792el Family of Metalloproteases
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                                                                                                                                                                           Non-A/Non-B/Non-C/Non-D/Non-E Hepatitis
Agents and Molecular Cloning Thereof
106
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/05980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,986
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 4600-0201.49
TELECOMMUNICATION INFORMATION:
TELEFANE: (415) 324-0880
TELEFAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 16;
100.0%; Pred. No.
ive 0; Mismatc
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                                                     RESULT 53
PCT-US95-05980-98/c
; Sequence 98, Application PC/TUS9505980
; GENERAL INFORMATION:
; APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08937931
Patent No. 5935792
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rooke, Jenny
APPLICANT: Yavari, Reza
APPLICANT: Xu, Tian
TITLE OF INVENTION: KUZ:
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 gccgcgagcggccgcg 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 base pairs
                                                                                                                                                                         TITLE OF INVENTION: Non-
TITLE OF INVENTION: Agen
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
  21 GCCGCGAGCGGCGCG 6
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GCCGCGAGCGGCCGCG
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
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GENERAL INFO
APPLICANT:
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APPLICANT:
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APPLICANT: Wages, John
APPLICANT: Zhang-Keck, Zhen-Yang
APPLICANT: Zhang-Keck, Zhen-Yang
APPLICANT: Young, LaVonne
TITLE OF INVENTION: No. 5859230-A/No. 5859230-B/No. 5859230-C/No. 5859230-D/No. 58
TITLE OF INVENTION: Agents and Molecular Cloning Thereof
NUMBER OF SEQUENCES: 106
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Length 252;
                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/611,757
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Pred. No. 2.2e+02;
0; Mismatches 0;
ore 16; DB 4; I red. No. 2.2e+02; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
  Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION BATA:
APPLICATION NUMBER: 08/246,985
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: US 025,396
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,493
FILING DATE: 30-UL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: SCH Clone SU7-8
                                                                                                                                                                                                                  Sequence 98, Application US/08611757 Patent No. 5859230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.5%; Soc
Best Local Similarity 100.0%; Pi
Matches 16; Conservative 0;
Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fabian, Gary R. REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 46(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 324 0880
TELEFAX: (415) 324 0960
INFORMATION FOR SEQ ID NO: 98
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            Kim, Jungsuh P.
                                                                             1478 aagaagtcagtaccca 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 gccgcgagcggcgcg 148
                                                                                                                199 AAGAAGTCAGTACCCA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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APPLICANT:
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us-09-434-382-3.oliq.rni

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Gaps

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GENERAL INFORMATION:
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
TITLE OF INVENTION: Characterization of mRNA Patterns
TITLE OF INVENTION: in Neurites and Single Cells for Medical Diagnosis and
TITLE OF INVENTION: Therapeutics
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFCATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,254
FILING DATE: No. 5958688ember 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CT/US95/14792
FILING DATE: No. 5958688ember 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: PENN-00219
TELECOMMUNICATION INFORMATION:
TELEFHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08848131 Patent No. 5958688
             TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                                  1881 caggaaggggctgaga 1896
                                                                                                                                                                                                                                                                                                            Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                   LINEAR
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MEDIUM TYPE: DISKETT
                                                                                                                                                  TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
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                                                                                                                                                                       STRANDEDNESS:
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US-08-334-254-7
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                                                                                                                                                                                                 TOPOLOGY
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n. 2.2e+02;
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
ATILE OF INVENTION: USE OF NURTITE LOCALIZED MRNAS FOR
TITLE OF INVENTION: MEDICAL DIAGNOSIS AND THERAPEUTICS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jame Massey Licata, ESQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,254
FILING DATE: HERWITh
                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,931
             ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jane Massey Licata, Esq. STREET: 210 Lake Drive East, Suite 201 CITY: Cherry Hill
                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08334254 Patent No. 5723290
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/ASENT INFORMATION:
ATAR: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFRENCE/POCKET NUMBER: B97-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 cttactttaaaggaaa 441
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
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73-08-937-931-9
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COUNTRY:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06418
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
Matches 16; Conservative
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MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 30303.40
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                                                                                  20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-507-016-8
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Sequence 8, Application US/08507016
Sequence 8, Application US/08507016
GENERAL INFORMATION:
APPLICANT: EVANS, HELEN F.
APPLICANT: STINE, JOHN
TITLE OF INVENTION:
HUMAN GALANIN, CDNA CLONES ENCODING
TITLE OF INVENTION:
HUMAN GALANIN AND A METHOD OF PRODUCING HUMAN GALANIN
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                     Gaps
                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
APPLICANT: James Eberwine, Marc Dichter, Kevin Miyashiro
ATILE OF INVENTION: USE OF NEURITE LOCALIZED MRNAS FOR
TITLE OF INVENTION: MEDICAL DIAGNOSIS AND THERAPEUTICS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Le
  Pred. No. 2.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14792
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16;
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tive 0;
Best Local Similarity 100.0%; P. Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEG ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                          1881 caggaaggggctgaga 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1881 caggaaggggctgaga 1896
                                                                                    184 CAGGAAGGGGCTGAGA 199
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Best Local Similarity
Matches 16; Conserv
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ZIP: 08002
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Gaps
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Sequence 4, Application PC/TUS9106418
GENERAL INFORMATION:
APPLICATION: Oklahoma Medical Research, Foundation, et al
TITLE OF INVENTION: Antigens Associated with Polymyositis
TITLE OF INVENTION: and with Dermatomyositis
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 575;
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COMPOTER: IBM PC Compatible
OPERATE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ore 16; DB 1; L red. No. 2.2e+02; Mismatches 0;
                                               COFFRANCE PATENT Release #1.0, Vers CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,016
FILING DATE: 25-JULY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,733
FILING DATE: 06-MAR-1993
APPLICATION NUMBER: PCT/AU92/00097
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT THRORMATION:
NAME: ERNEY, BARBARA G:
REGISTRATION NUMBER: .30,377
REFERENCE/DOCKET NUMBER: .30,377
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Kilpatrick & Cody STREET: 100 Peachtree Street
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                                                                                                                                                                                                             DB 3; Len.,
0, 2.2e+02;
0; Indels
                                                                                                                                                                                                                           Length 609;
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Pred. No. 2.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                             Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/911,319A FILING DATE: Aquast 14, 1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-911-319A-2; Sequence 2, Application US/08911319A; Patent No. 5968798
                                                                                                                                                                                                                           Query Match 0.5%; Soc
Best Local Similarity 100.0%; Pi
Matches 16; Conservative 0;
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Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Muenzen, Colette C.
REGISTRATION NUMBER: 39,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: 650-855-0555
                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                     2740 gggccaggaggctgcc 2755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2402 gegggagetgeggeag 2417
             : 609 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                           564 GGCCAGGAGGCTGCC 549
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650-845-4166
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                                                                                                                                                   163..609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                         linear
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US-08-911-319A-2
                                                                                                                               ) NAME/KEY: CDS
; LOCATION: 163
US-08-338-579A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
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                                     TYPE:
                                                                                                               FEATURE
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Patent No. 6068975
CENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
TITLE OF INVENTION: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/338,579A
FILING DATE: June 17, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; L
2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 0575/44011-A-PCT-US TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16; DB 4; Pred. No. 2.26 0; Mismatches
     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/579023
FILING DATE: 09-101-1990
ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
TELEPHONE: 404-572-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 94:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 278-04(
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
                                                                                                                                                                                                           TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               LENGTH: 578 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       955 ctggtgctgcttttgt 970
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Best Local Similarity 100.
Matches 16; Conservative
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FRAGMENT TYPE: N-termin:
ORIGINAL SOURCE:
ORGANISM: Homo sapien
19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 CIGGIGCIGCITITGT 7
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                                                                                                                                                                                                                                                                                                             Sirain Topology: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: JH2
TISSUE TYPE: Sera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSULT 60
S-08-338-579A-94/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UI
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                                                                                                             COMPETATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,738
FILING DATE: 19920330
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOEFNEY JF., Dennis R.
REGISTRATION NUMBER: 30,914
REGISTRATION NUMBER: 30,914
REJERRENCE/POCKET UNBER: 30,914
RELECOMMUNICATION INFORMATION:
TELEPRAK: (314)537-6099
TYNTELEFRAK: (314)537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CUBRENT APPLICATION DATA:
FILLATION NUMBER: US/07/789,738
FILING DATE: 19920330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16; DB 1; Lv
Pred. No. 2.2e+02;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 38-21(10540)A TELECOMMUNICATION INFORMATION: TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Beachy, Roger N.
APPLICANT: Bhattacharyya, Maitrayee
TITLE BINVERION: Plant Promoter
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 64
US-07-789-738-5
: Sequence 5, Application US/07789738
: Patent No. 5824857
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOEINER JI., DEDNIS R.
REGISTRATION NUMBER: 30,914
                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; (
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) US-07-789-738-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1842 gtcctgcaccacatca 1857
                                                                                                                                                                                                                                                                                                                                                                TELEFRAX: (314)537-6047 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 714 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 GICCIGCACCACATCA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7/73 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                    ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: FlOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: St. Louis
STATE: Missouri
COUNTRY: USA
Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                     COUNTRY:
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STREET: 700 Chesterfield Parkway No. 5824857th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ' 0.5%; Score 16; DB 3; I 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPENATING SYSTEM: DOS
SOFTWARE: FastERQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Muenzen, Colette C.
REGISTRATION NUMBER: 39,784
REFERENCE/DOCKET NUMBER: PF-0363 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 560-855-0555
TELECAX: 660-845-4166
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 654 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Beachy, Roger N.
APPLICANT: Bhattacharyya, Maitrayee
TITLE OF INVEWION: Plant Promoter
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/09/352,619
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APPLICATION NUMBER: 08/911,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
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                                                                                                                     Sequence 2, Application US/09352619
Patent No. 6084070
GENERAL INFORMATION:
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101 GCGGGAGCTGCGGCAG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 16; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: THP1NC
CLONE: 2447829
TS-09-352-619-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           94304
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                                                                                                                                                                                                                                                                                                                                               CITY: Pa]
STATE: C!
COUNTRY:
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3-07-789-738-3
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Sequence 128, Application US/08906769 Patent No. 6077687
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LOCATION: 1..762
OTHER INFORMATION:
OTHER INFORMATION:
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COTHER INFORMATION:
US-08-906-769-128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                         US-08-906-769-128/c
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                                                                                                                                                       Length 773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schulein, Martin
APPLICANT: Andersen, Lene N.
APPLICANT: Andersen, Soren F.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Lange, Lene
APPLICANT: Inare, Lene
APPLICANT: Inare, Michiko
APPLICANT: Thara, Michiko
APPLICANT: Taxaqi, Shinobu
TITLE OF INVENTION: No. 6001639el Endoglucanases
NUMBER OF SEQUENCES: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER: REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                       Score 16; DB 1; Le
Pred. No. 2.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; DB 3; Le
Pred. No. 2.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEI/AGENT.
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/08651136C Patent No. 6001639
                                                                                                                                                       Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 808 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLGGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          1842 gtcctgcaccacatca 1857
                                                                                                                                                                                                                                                                                    484 GICCIGCACCACATCA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear . MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 37..714
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S-08-651-136C-15
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75-08-651-136C-15
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1409 teccaaettecageag 1424 |||||||||||||||||

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"At pos. bp 453, change A to
"At pos. by 453, change A to M; at 457, A to M; at 456, G to V; at 457, A to M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M; at 454, change G to V; at 456, G to V; at 45
460, A to R; at 470, G to S; at 493, A to R. A:
136, 152, 153, 154, 157 and 165, substitute Xaa
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiedjer, Gary
APPLICANT: Stiedjer, Gary
APPLICANT: Silver, Gary
TITLE OF INVENTION: FIEA PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: FIEA PROTEINS, NUCLEIC ACID
TITLE OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 16; DB 3; L. 00.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
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APPLICATION NUMBER: US/08/906,769
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/639,075
FILING DATE: 24 APR-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-
TELECOMMUNICATION INFORMATION:
TELEPAX: (303) 863-0700
TELEPAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 815 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy 1478 aagaagtcagtaccca 1493
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AAGAAGTCAGTACCCA 166
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US-08-906-616-128/c
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No. 60016390 No. 6001639disk of No. 6001639th America, Inc.
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                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORFWARES: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATONNEY/AGERT INPOMMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/POCKET NUMBER: 2618-25-C2
TELEFONMINICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFONE: (303) 863-9700
TELEFAX: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lange, Lene
APPLICANT: Nielsen, Ruby I.
APPLICANT: Ihara, Michiko
APPLICANT: Takagi, Shinobu
TITLE OF INVENTION: No. 6001639el Endoglucanases
NUMBER OF SEQUENCES: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 3; I
Pred. No. 2.2e+02;
MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 405 Lexington Avenue, 64th Floor
New York
                                                               ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08651136C; Patent No. 6001639; GENERAL INFORMATION:
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100.0%; Pre
0;
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Andersen, Lene N.
Lassen, Soren F.
Kauppinen, Markus S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 815 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION:
US-08-639-075A-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1.762
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                      Denver
: Colorado
RY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                             COUNTRY: UZIP: 80203
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APPLICANT:
APPLICANT:
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                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 69
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                                       APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Keith E.
APPLICANT: Frank, Glann R.
APPLICANT: Frank, Glann R.
APPLICANT: Stiegler, Gary
APPLICANT: Sliver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF NUMBER OF SEQUENCES: 190
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100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                     ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRAINON NUMBER: 32,020
REFERENCE/DOOKET NUMBER: 2618-25-C2-3
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-0223
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 815 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                      E: Sheridan Ross P.C.
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
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\sigma 5-08-639-075A-128/c
Sequence 128, Application US/08639075A
Patent No. 6150125
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100.0%; Pre
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Rushlow, Keith E.
Wu Hunter, Shirley
Frank, Glenn R.
Stiegler, Gary
Gaines, Patrick J.
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ADDRESSEE: Sheridan I
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LOCATION:
1..762
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
CTHER INFORMATION:
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                                                                                                                                                                                                                                                                                               CITY: Denver
STATE: Colorado
COUNTRY: USA
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APPLICANT: Grieve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 13
                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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0.5%; Score 16; DB 3; Length 1048; 100.0%; Pred. No. 2.2e+02;
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APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 81, Application US/08933750C Patent No. 5932442 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555 TELEFRAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bandman, Olga
Shah, Purvi
Au-Young, Janice
                                 INFORMATION FOR SEQ ID NO: 17 SEQUENCE CHARACTERISTICS: LENGTH: 1048 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     1409 teceaacttecageag 1424
                                                                                                                                                                                                                                                                                                                                                                                                                          553 TCCCAACTTCCAGCAG 568
                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: Septemb
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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13..906
                                                                                                                                                                                MOLECULE TYPE: CDNA
                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94304
                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-651-136C-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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STATE:
                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 3; Length 1031;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6001639el Endoglucanases
NUMBER OF SEQUENCES: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
                                                                                                             AFFLING DATE: 21-MAY-1996
CLASSIFFIAMIL: 21-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/08651136C Patent No. 6001639
                                                                                                                                                         CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: LAMBLIS, ELIAS J. 128
RECISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
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Kauppinen, Markus S.
Lange, Lene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: Lange, Leue

R: Nielsen, Ruby I.

T: Ihara, Michiko

T: Takagi, Shinobu
                                                                                                                                                                                                                                                                                                  TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schulein, Martin
Andersen, Lene N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1409 teceaacttecageag 1424
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11..889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
US-08-651-136C-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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APPLICANT:
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Score 16; DB 2; Length 122
Pred. No. 2.2e+02;
---+ohes 0; Indels
                                                                                                                            Sequence 4, Application US/08739485
Patent No. 5863898
GENERAL INFORMATION
APPLICANT: GOli, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN LIM PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/739,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SISTEM: DOS
SOFTWARE: FASTSEO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-360-758-1/c
; Sequence P, Application US/08360758
; Patent No. 6074863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: IBM Compatible
DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Pathar, Shamkant A
APPLICANT: Egel-Mitani, Michi
APPLICANT: BOCO, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1225 base pairs
TYPE: nucleic acid
1835 ccaggaggtcctgcac 1850
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Clausen, Ib G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER:
FILING DATE:
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LIBRARY: Consensus
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CLASSIFICATION:
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IMMEDIATE SOURCE:
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                                                                                                RESULT 73
US-08-739-485-4
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                                                                                                                0.5%; Score 16; DB 2; Length 1152; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SUFUARRE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0356 US
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Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                     Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 1152 base pairs
TYPE: nucleac acid
STRANDEDNESS: single
                                                                                                                                                                                            2168 ccaagccatcagcgtg 2183
                                                                                                              Query Match
Best Local Similarity 100.C
Matches 16; Conservative
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IMMEDIATE SOURCE:
LIBRARY: BLADNOT03
CLONE: 1602473
                    LIBRARY: BLADNOT03
CLONE: 1602473
:S-08-933-750C-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                            ::S-09-234-613-81/c
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ZIP: 94304
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Gaps

Length 1225;

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DB 3; Length 1333; 2.2e+02;
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APPLICANT: Guegler, Karl J.
APPLICANT: Tue, Henry
APPLICANT: Lal, Pereti
TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
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100.0%; Pr.
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillman, Jennifer L.
                                                          NAME: Brook, David E.
REGISTRATION NUMBER: 22,59;
REFERENCE/DOCKET NUMBER: B.
TELECOMMUNICATION INFORMATION
                                                                                                                                     TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Diskette
IBM Compatible
                                                                                                                                                                                                                             LENGTH: 1333 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        534 gaactggctgtgcggc 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650-845-4166
                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                     CDS
58..840
                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-889-425-3
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lim, Bing
APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
ATTLE OF INVENTION: A Lysosomal-Associated Multispanning
TITLE OF INVENTION: Membrane Protein, LAPTM5 and a Nucleic Acid Encoding
TITLE OF INVENTION: LAPTM5
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                         ADDRESSEE: No. 60748630 No. 6074863disk of No. 6074863th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
                   C. ANTARCTICA LIPASE AND LIPASE VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1329;
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                                                                                                                                                                                                                                                                                 SOFTWARE: PATENTIN FOLDS/MS DO. VERSION #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,758
FILING DATE: 22-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK PCT/DK93/00225
FILING DATE: 03-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/889,425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; L6
2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                               COUNTRY: United States of America ZIP: 10174-6401
COMPUTER READABLE FORM:
                                                                                                                                                                                                                             MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08889425
Patent No. 6153403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
APPLICANT: Hansen, Mogens T
TITLE OF INVENTION: C. ANTAF
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Two Militia Drave
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Lexington
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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ADDRESSEE:
ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                         Length 1341;
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                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Preparation of Acariogenic Sugar TITLE OF INVENTION: Substitutes NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Le...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                       DB 3; Le
2.2e+02;
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ilarity 100.0%; Pred. No.
Conservative 0; Mismatcl
                                                                                                                                                                       Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/374,155A FILING DATE: 18-74N-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08374155A Patent No. 5786140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FORMAN, DAVIG'S
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 0563
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     0.5%; Scallarity 100.0%; P: Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
US-08-374-155A-7
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Schiweck, Hubert
Kunz, Markwart
APPLICANT: Munir, Mohammed
LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1362 base pairs
                                                                                                                                                                                                                                      2624 cacggtcccccaggag 2639
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                                                                                                                                                                                                                                                                       794 CACGGTCCCCCAGGAG 779
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                       BRAITUT21
                                                      linear
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Best Local Similarity
Matches 16; Conserva
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Best Local Similarity
Matches 16; Conservi
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                                                  TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT
CLONE: 2522306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Wash
STATE: D.C
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15-08-374-155A-7
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Length 1362;
                                                                                                                                                                        TITLE OF INVENTION: Preparation of Acariogenic Sugar TITLE OF INVENTION: Substitutes NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takegi, Shinobu
APPLICANT: Takegi, Shinobu
APPLICANT: Boominathan, Karuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
OVERESPONDENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3315
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; LE
2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/374,155
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FORMAL, DAVIG S
REGISTRATION NUMBER: 33,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16;
Pred. No.
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; Patent No. 5667990
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100.0%; Pro
Sequence 7, Application US/08785396 Patent No. 5985622
                                                                                                                                                                                                                                                                                                     1300 I Street, N.W.
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; MOLECULE TYPE: DNA (genomic)
US-08-785-396-7
                                                                                        Klein, Kathrin
Schiweck, Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (202) 408-4000
                                                             APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Schiweck, Hubert
Kunz, Markwart
APPLICANT: Munir, Mohammed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                Washington
                                             GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COlin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
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(202)672-5399
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                       LENGIH: 1389 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3000 h CTTY: Washington, D.C.
                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 16; Conservi
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                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
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No. 5667990o No. 5667990disk of No. 5667990th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Egel-Mitani, Michi
APPLICANT: Borch, Kim
APPLICANT: Clausen, Ib G
APPLICANT: Hansen, Mogens T
TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1389;
                                                                                                                                                COMPOURE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REGISTRATION NUMBER: 31,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; L6
2.2e+02;
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TS-09-111-556A-1/c

Sequence 1, Application US/09111556A

Patent No. 6020180
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                405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Candida antarctica
INDIVIDUAL ISOLATE: DSM 3855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pathar, Shamkant A
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 16; Conservative
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COMPUTER READABLE FORM:
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: No. 60201
STREET: 405 Lexingto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..1389
                                                                                          10174-6201
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          STREET: 400
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                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
5-08-458-023B-1
                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
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Human Cholesterol
Jase, Method of Production and Use Thereof
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/135,510
FILING DATA:
CLASSIFICATION: 424
                                                          FILLING LAME: ac LCC. LCC.

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DR PCT/DK93/00225

ATTING DATE: 03-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DÓCKET NUMBER: 33,748

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Foley & Lardner
3000 K Street, N.W., Suite 500
22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHIANG, John Young Ling
TITLE OF INVENTION: Truncated Human
TITLE OF INVENTION: 7a-Hydroxylase,
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08135510 Patent No. 5420028
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Conservative 0;
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APPLICANT: JOYCE, JAMES G.
APPLICANT: GEORGE, HUGH A.
APPLICANT: HORMANN, KATHRYN J.
APPLICANT: HORMSHN, KATHRIN U.
APPLICANT: NEEPER, MICHAEL P.
APPLICANT: NEEPER, MICHAEL P.
APPLICANT: NEEPER, MICHAEL P.
APPLICANT: NEEPER, MICHAEL P.
                                       GENERAL INFORMATION:
APPLICANT: CHIANG, John Young Ling
TITLE OF INVENTION: A-Hydroxylase and Methods of Using It
TITLE OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITT: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1524;
                                                                                                                                                                                                                                                                                                                                                                      URENATING SYSTEM:

URENATING SYSTEM:

URENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,953

FILING DATE: O'-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/361,458

FILING DATE: 1-DEC-1994

PRIOR APPLICATION NUMBER: US 08/135,511

FILING DATE: 13-OCT-1993

PRIOR APPLICATION NUMBER: US 08/135,510

FILING DATE: 13-OCT-1993

PRIOR APPLICATION NUMBER: US 08/135,510

FILING DATE: 13-OCT-1993

APPLICATION NUMBER: US 08/135,510

FILING DATE: 13-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: SANDERCOCK, COLIN G.

REGISTRATION NUMBER: 31,298

REFERENCE/OCKET NUMBER: 18748/219 HOCE

TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; DB 1; L
No. 2.2e+02;
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                                                                                                                                                                                                                                            COUNTY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
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Sequence 1, Application US/08409122
Patent No. 5820870
GENERAL INFORMATION:
APPLICANT: JOYCE, JAMES G.
APPLICANT: GEORGE, HUGH A.
Sequence 4, Application US/08477953
Patent No. 5677159
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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Best Local Similarity
Matches 16; Conserve
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Patent No. 5650286
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genomic DNA of Human Cholesterol
TITLE OF INVENTION: 7a-Hydroxylase and Methods of Using It
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
0.5%; Score 16; DB 1; Length 1524;
100.0%; Pred. No. 2.2e+02;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16; DB 1; L
Pred. No. 2.2e+02;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPLICATION NUMBER: US/08/483,852
FILING DATE: US-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/361,458
FILING DATE: 21-DEC-1994
PRIOR APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PRIOR APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: AND ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COIN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5°,
100.0%; Piv
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TELEFAX: (202),
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TUPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET, NUMBER: 18
IELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499 caatcaaaatatttc 514
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                                                                                                             252 CAATCAAAATATTTC 237
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Best Local Similarity 100.
Matches 16; Conservative
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
                        Local Similarity
                                                                                                                                                                                       RESULT 82
TS-08-483-852-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TS-08-483-852-4
                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: 1
STATE:
  Query Match
                          Best Loca
Matches
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Gaps

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Gaps
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US-08-477-952-4/C

Sequence 4, Application US/08477952

Patent No. 5851780

GENERAL INFORMATION:
TITLE OF INVENTION: Genomic DNA of Human Cholesterol
TITLE OF INVENTION: 7a-Hydroxylase and Methods of Using It
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1524;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: RC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,952
FILING DATE: 07-JUN-1995
PRICK APPLICATION NUMBER: US 08/361,458
FILING DATE: 21-DEC-1994
PRICK APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PROK APPLICATION DATA:
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
PROK APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16; DB 2; L4
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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'APPLICATION NUMBER: US 08/135,510
                                                                                                                                                                     NAME: CARTY, CHRISTINE E
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELECHONE: 908-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; (
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1524 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 cctgcaggtggtggca 242
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                     TELEPHONE: 908-594-67
TELEFAX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                 APPLICATION NUMBER:
FILING DATE: 22-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-408-669-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N<sub>O</sub>
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Patent NO. 5840306
GENERAL INFORMATION:
APPLICANT: HOFMANN, KATHRIN U.
APPLICANT: JANSEN, KATHRIN U.
APPLICANT: NEEPER, MICHAEL P.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
               CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000 CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000 CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16; DB 1; L
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,122
                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/408,669
FILING DATE: 22-MAR-1995
ATTONEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E
REGISTRATION NUMBER: 36,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: DOS
FastSEQ Version 1.5
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REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISKETTE DESCRIPE OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 CCTGCAGGTGGTGGCA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 cctgcaggtggtggca 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                          COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIN
  NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UR-08-409-122-1
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Gaps
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       Length 1713;
                                                                                                                                                                                                                                                                                                                                                     BACTERIAL CATABOLISM OF CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,452A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                        3: FISH & RICHARDSON P.C. 4225 Executive Square, Suite 1400
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              RESULT 88
US-08-600-452A-5/c
; Sequence 5, Application US/08600452A
; Patent No. 5985644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08467948A; Patent No. 5998164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
       Ouery Match 0.5%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0
                                                                                                                                                                                                                                                                                                 APPLICANT: CHITLARU, EDITH
APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHARLES
TITLE OF INVENTION: BACTERIA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) US-08-600-452A-5
                                                                                                                                                                                                                                                                                    KEYHANI, NEMAT O.
                                                                                                                                                                                                                                                  ROSEMAN, SAUL
BASSLER, BONNIE
                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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STREET: 422_
TTW: La Jolla
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-467-948A-1
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 89
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                                                                                                                                                                                                                                                                                                     Length 1524;
                                                                                                                                                                                                                                                                                   DB 2; Len.,
7. 2.2e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHITLARÜ, EDITH
APPLICANT: ROME, CHRIS
APPLICANT: YU, CHRIS
TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4130/206916
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                                                                                                                                                                                                                                                                                    0.5%; Scc.
100.0%; Pre
0;
ATTORNEY AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 1874!
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELERAX: (202)672-5399
TELERAX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISICS:
LENGTH: 11524 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOBBS, ANN S.
REGISTRATION NUMBER: 36,830
REFERENCE/DOCKET NUMBER: 4130,
TELECPHONE 202-861-3000
TELEPHONEX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'S-08-386-727-5/c
Sequence 5, Application US/08386727
Patent No. 5792647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEMAT O
                                                                                                                                                                            LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1713 base pairs
                                                                                                                                                                                                                                                                                                 Ouery Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                    499 caatcaaaatatttc 514
                                                                                                                                                                                                                                                                                                                                                                                       252 CAATCAAAATATTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucletc acid
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                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                              TOPOLOGY:
:S-08-477-952-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
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Sequence 13, Application US/07688352C
Patent No. 5527896
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: FLOPPY DISK
COMPUTER: FLOPPY DISK
COMPUTER: FLOPPY DISK
COMPUTER: PATENTIN RELEASE #1.0, VERSION #1.30
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, BRIC K
REGISTRATION NUMBER: 36.688
REFERENCE/DOCKET NUMBER: 36.688
REFERENCE/DOCKET NUMBER: 36.688
REFERENCE/DOCKET NUMBER: 36.688
REFERENCE/DOCKET NUMBER: 1488:1140002/EKS/KLM
TELECOMMULICATION:
TELEPHONE: 200-311-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 16; DB 3; I
100.0%; Pred. No. 2.3e+02;
: 1100 NEW YORK AVE., NW, SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19910419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      824 agcaaaggagatgggc 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 AGCAAAGGAGATGGGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-467-947A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                             TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein TITLE OF INVENTION: Coupled Receptor GPR2 NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein IIILE OF INVENTION: Coupled Receptor GPR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1713;
                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                                        COUNTRI.

ZIP: 20005

ZIP: 20005

COMPUTER FEADABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATEMITN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,948A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PELICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/POCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAS: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3e+02;
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GENTZ, REINER
BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
                       GENTZ, REINER
BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08467947A Patent No. 6090575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHRACTERISTICS: LENGTH: 1713 base pairs TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                824 agcaaaggagatgggc 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 AGCAAAGGAGATGGGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
116..1003
                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIF
APPLICANT: NI, JIAN
APPLICANT: GENTZ, F
APPLICANT: SULT, CP
APPLICANT: SUTTON I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSULT 90
S-08-467-947A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
74-08-467-948A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF
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RESULT 93
US-09-146-2494-13
US-09-146-2494-13
Sequence 13, Application US/09146249A
Patent No. 606240
GENERAL INFORMATION:
APPLICANT: Wighler, Michael H.
APPLICANT: Colicelli, John J.
ITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
STREET: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Illinois
CONTY: Chicago Sears Tower, 233 South Wacker Drive
CITY: Chicago States of America
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1721;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 16; DB 2; I
100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                  TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-648
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 13
SEOURNCE CHARACTERISTICS:
LENGTH: 1721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2731 cacagccgcgggccag 2746
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 CACAGCCGCGGGCCAG 281
                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 66.1274
US-08-474-379C-13
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; LOCATION: .66..1274
US-09-146-249A-13
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                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wigler, Michael H.
APPLICANT: Wigler, Michael H.
APPLICANT: Wigler, Wichael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
CITY: Chicago
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
CITY: Chicago
STREET: 111nois
COUNTRY: United States of America
COMPUTER READBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: DATE: O'DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 19-MAR-1994
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
AND ATTORNEY/AGENT INFORMATION:
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No. 2.3e+02;
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBR: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, MICHAEL F.
REGISTRATION NUMBER: 2547
REFERENCE/POCKET NUMBER: 27805/30197
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
TELEPK: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1721 base pairs
TYPE: NUCLEIC ACID
STRANDENCEY: 51091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .S-08-474-379C-13
Sequence 13, Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.5%; Sc
Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 60...
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United States of America
                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 1721 base pairs NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                              CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 60...
PCT-US91-02714-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                         Gaps
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APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1721;
 Length 1721;
                                                                                                                                                                                                                                                                                                                                                                                  3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-AMR-1994
CLASSIFICATION ATA:
PRIOR APPLICATION DATA:
DB 3; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 16; DB 3; L
.00.0%; Pred. No. 2.3e+02;
0.5%; Score 16; DB 100.0%; Pred. No. 2.3 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APF-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSULT 95
CT-US91-02714-13
Sequence 13, Application PC/TUS9102714
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
                                                                                                                                                                                                          Sequence 13, Application US/08206188B Patent No. 6100025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1721 base pairs
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                                                                               2731 cacagccgcgggccag 2746
 Query Match
Best Local Similarity 100.C
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                 266 CACAGCCGCGGGCCAG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66..1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-08-206-188B-13
                                                                                                                                                                                        3-08-206-188B-13
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16; DB 4; Length 1721; Pred. No. 2.3e+02;
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US-08-481-814A-2

Sequence 2, Application US/08481814A

Patent No. 5869040

PATENT NO. SABOROM

TITLE OF INVENTION: GENE THERAPY METHODS AND COMPOSITIONS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Biogen, Inc.

STREET: 14 Cambridge Center

CITY: Cambridge Center

STREET: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URFERENTION SISTEM:

URRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 19910419

CLASSIFICATION 1435

PRIOR APPLICATION NUMBER: 07/V511,715

FILING DATE: 20-APR-1990

ATTONNEY/AGENT INFORMATION:

NAME: BOTUN, MICHAEL E.

REGISTRATION NUMBER: 25447

REGISTRATION NUMBER: 25447

REGISTRATION NUMBER: 25447

REGISTRATION NUMBER: 25447

REGISTRATION NUMBER: 25467

TELEPHONE: (312) 346-5750

TELEFAX: (312) 346-5750
                                                                                                                                                                                                                                                                                            STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: COTIEY, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEIN KINASE AND KINASE INHIBITORS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                               Length 1790;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                 Score 16; DB 2; L
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARR: FastSDO for Windows Version 2.0
SUGRENT APPLICATION DAR:
APPLICATION NUMBER: US/09/231,529
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0429 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/977,816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09231529 Patent No. 6096308 GENERAL INFORMATION:
               REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEFAHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

WEDIUM TYPE: DOSACTE

DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 1977 base pairs
                                                                                                                                    1790 base pairs
                                                                                                                                                                                                                                                                                   Ouery Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                    nucleic acid
EDNESS: double
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: sing
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SOFTWARE: FastSE
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                                                                                                                                                                                           linear
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; CLONE: 3453694
US-09-231-529-2
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                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                       ; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-993-228-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,814A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB : Fred. No. 2.30 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat_peptide
LOCATION: 429.1739
OTHER INFORMATION: /product= "E2F-2"
S-08-481-814A-2
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87 CambridgePark Drive
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100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A
REFERENCE/DOCKET NUMBER: A00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2000
TELEFAX: 617-679-2000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           CDNA to mRNA
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                                                                                                                                                                                                                                                               1766 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                CELL LINE: HeLA FEATURE:
                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.5
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 GCCGCGGCCAGGAGG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics
STREET: 87 Cambridge
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: HOM
                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02140
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0.5%; Score 16; DB 1; Le
100.0%; Pred. No. 2.3e+02;
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Job time: 24889 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%,
100.0%; Pre
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: COPPOLA, JOSEPH A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 1910
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-6734
TELEPHONE: 732-594-4720
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2069 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1298 AGATTTTGGCTGAAGA 1313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conservi
                                                                                                                                                                                                                                                                                                                                               linear
                                           ö
                                           Gaps
                                           ö
0.5%; Score 16; DB 3; Length 1977;
100.0%; Pred. No. 2.38+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                 APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SMADI EXPRESSION
CURRENT APPLICATION NUMBER: US/09/255,911
CURRENT PILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 46
LENGTH: 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ECONOCIENT, MODIMINE APPLICANT: FOOR, FORTEST APPLICANT: KAHN, Jennifer, - PARENT, S.A. APPLICANT: WARNINAN, Jean, - RAMADAN, N.M. APPLICANT: WARNINAN, Jean, - RAMADAN, N.M. APPLICANT: ONISHI, Janet, - SHEI, Gan-Ju TITLE OF INVENTION: SYNTHASE SUBUNITS NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: JOSEPH A. COPPOLA - MERCK & CO., INC
126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Le
2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASISEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/619,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOUGLAS, Cameron M.
CHREBET, Gary L.
CLEMAS, Joseph
EL-SHERBEINI, Mohammed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08619554
Patent No. 5821353
                                                                                                                                                                                                                     Sequence 1, Application US/09255911
Patent No. 6013522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1077 atggccccagcatctg 1092
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                                                                                  1462 cagccccagcagagaa 1477
    Query Match 0.5%
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                         419 CAGCCCCAGCAGAA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (433)..(1830)
:3-09-255-911-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                        3-09-255-911-1
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Length 2069;

em_esthum6:*
em_esthum7:*
em_esthum8:*

em_esthum10: em_esthum11: em_esthum12:

em_esthum13: em_esthum14: em_esthum15:

em_esthum16

em_esthum20: em_estin1:* em_estin2:*

em_estin3: em_estin4: em_estov1: em_estp11: em_estp12: em_estp13:

em_estp14:

em_estro4:

em_estro6

em_estro13

gb_est41: gb_est42:

9b_est43: 9b_est44: 9b_est45: 9b_est46: 9b_est47: 9b_est48: 9b_est48:

em_esthum19

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February 18, 2001, 05:22:53; Search time 2148.29 Seconds (without alignments) 9648.673 Million cell updates/sec
                                                                                                                                                                                                  1 cgcgggcgtaggtgaccggc.....aataaagattgagtttgcaa 2958
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                 7991742 seqs, 3503743858 residues
                                                                                                                                                                                                                                                                                                                                                otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sost-processing: Listing first 100 summaries
                                                             .M nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                  OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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2958
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em_estfun:
em_esthuml
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                                                                                                                                                                 Title:
Perfect score:
Requence:
                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                    Gord size :
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                                                                                                Run on:
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em_estom1: em_estom2:

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em_estro15:*
em_estro16:*
em_estro17:*
em_estpl6:*
em_estpl7:*
em_estpl8:*
em_estro14:*
                                                                em_estro18:
                                                                         em_estro19:*
gb_est58:*
                                                                                                   gb_est60:
gb_est61:
gb_est62:
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em_gss9:*
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gb_gss12:
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gb_gss15:
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gb_gss19:
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gb_gss21:
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gb_est64:
gb_est65:
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jb_est79:
jb_est80:
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gb_est77
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gb_est75
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em_gss7:
em_gss8:
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                                                                                                                                                                                                                                  jb_est82
jb_est83
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                                                                                                                                                                                                                                                    b_est8
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| results predicted by 1 to the score of the 5 summaries summaries summaries 5 summaries 5 summaries 5 summaries 5 summaries 6 s | |
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| gb_gss25:* gb_gss26:* gb_gss26:* gb_gss26:* gb_gss26:* gb_gss26:* gb_gss26:* gb_gss26:* gb_gss26:* gb_gss26:* gb_gss27:* | 3 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 |
| Pred. No. is the score greater than the score | |
| R R R R R R R R R R R R R R R R R R R | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 |

| FEATURES 1676 /organism="Homo saplens" /db_xref="taxon:9606" /clone="IMAGE:3503184" /clone="IMAGE:3503184" /tlssue_type="neuroblaston"/hab_host="Deutoblaston"/hab_host="Deutoblaston"/hab_host="Deutoblaston"/hote="Organ: brain: Vector V | ECORI, CDNA made by oligon cloned into ECORI/Xhol sit adaptor: GGCAGGAG(G). Lil in the laboratory of Geral California, Berkeley) usin (Stratagene) and Supersci Note: this is a NIH,MGC Li BASE COUNT 154 a 207 c 176 q 139 | tch 22.9%; Score 676 al Similarity 100.0%; Pred. No 676; Conservative 0; Mismat | Oy 1143 acccagcacttggtcctgaatgagaactgtgctcacacaca | Db 61 ATTCAAACCCAGCTCAACCTCATCCCCGGACATC Qy 1263 tgtaagaaggagggccccaccctcagtgtgcccatg Db 121 TGTAAGAAGGGGCCCCCCCCCCCACTGGTGTGTTTTTTTT | Oy 1323 taccagctccgtcccaggaggagtggcagaggattgragatggtcll |
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| AA635046 ab48b06.r AA994126 ou38b06.s BB744876 601576324 AL033108 ow98908.s AW592223 hf41a01.x AA716607 z968907.s AA311855 EST182568 | A1991599 WS18C04.x BE938229 WS18C04.x BE938229 CM4-TN006 AA838624 O C91f04.s AW889463 RC6-NT002 H22087 y134C04.r1 BE409312 601300940 A1201492 qs74b03.x AR188525 AF188525 | AA522537 n138e08.s AA522537 n138e08.s AA528608 on75503.s T34024 EST61387 Hu A1357786 qu98d07.x BE515669 601279347 | AA23-352 & LESGIL: 5 AA180479 tu42d02.x AW296524 UI-H-BW0- N36229 yy30c04.s1 AW211765 xu16f03.x AW247380 2820640.5 | AA504146 aa59e06.s AA504146 aa59e06.s W37591 zc10f03.r1 R51138 yg71c08.r1 A1141263 qa46h05.s AA346268 EST52407 | A10318 y147e10.s1 A103318 y147e10.s1 A103342 0x02d12.s BE619874 601473130 T72963 yc65b06.r1 |
| 461 10 AA635046 364 87 AW175581 457 14 AA994126 984 135 BE744876 410 15 AN592223 461 92 AW592223 479 11 AA716607 501 5 AA311855 | 137 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 141 141 143 145 110 | * 68 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | 146 A 164 A 164 A | 147 141 151 140 145 |
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(base; 1 to 676)

National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: Robert Strausberg (aih. gov.
Tel: (31) 496-1550

Email: Robert Strausberg (aih. gov.
Tel: (31) A96-1550

Email: Robert Strausberg (aih. gov.
Tonact: Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LALL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCMAN76 row: d column: 01
High quality sequence stop: 672.
                                             BE260495 676 bp mRNA EST 13-JUL-2000 601150702F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503184 5' mRNA sequence.
BE260495' GI:9131807
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/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: CoRI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following Site_10nd into EcoRI/XhoI sites using the following Site_2: Lin the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHHMGC Library."
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600943455T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960077 3'
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                                                                                                                                                                                                                                                                                                                                                                                            National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert-Strausbergenih.gov
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/tissue_type="rhabdomyosarcoma"
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100.0%; Pred. No. v,
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/note="Organ: brain, Vector: porB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/AhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM313 row: a column: 13
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                                                                                                                                               351 AGGCTGTGTGTCTTCTGCCCCACGCACGCACCGTATCTGCCCCTCCTTGCTGGTAGAAGC
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/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
/clone="IMAGE:3628308"
/clone=lib="NIH_MGC_19"
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Location/Qualifiers
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/tissue_type="neuroblastoma" //tissue_type="neuroblastoma" //tissue_type="neuroblastoma" //tab_host="neuroblastoma" //tab_host="neuroblastoma; vector: poTB7; Site_1: XhoI; Site_2: EcoRI: cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
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                 /clone="IMAGE:3629028"
/clone_lib="NIH_MGC_19"
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1 (bases 1 to 692)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can.be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl,ggov. Plate: LLCW314 row: o column: 13
High quality sequence stop: 600.
Location/Qualifiers
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                                                                                                               1203 attcaaacccagctcaacctcatccacccggacatcttccccctgctcaccagtttccgc 1262
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601298656F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:3629028 ;
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0; Mismatches
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
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AUTHORS TITLE JOURNAL

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/note="Corgan: skin: Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally
cloned into ECORI/XhoI sites using the following 5/
adaptor: GGCACGAG(G). Size-salected >SOODP for average
insert size 1: 8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies)."
175 c 199 g 106 t
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM280 row: n column: 04
High quality sequence start: 18
High quality sequence stop: 611.
Location/Qualifiers
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                      1 (bases 1 to 627)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                            Unpublished (1999)
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                                            AUTHORS
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/note="Organ: lung; Vector: poTBF; Site_1: XhoI; Site_2: ECORI; CDNA made by oliqo-dT priming. Directionally cloned into EcorI/XhoI sites using the following 5′ adaptor: GGOACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Xit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 761)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM802 row: p column: 14
High quality sequence stop: 761.
Location/Qualifiers
1. 761
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2625 acggicococaggaggcagoicaggalaggiggiaiggagoigigcogaggoilggg 2581
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                             496 ACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGGTATGGAGCTGTGCCGAGGCTTGGG
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 4.2e-268;
O; Mismatches 1;
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/db_xref="taxon:9606"
/clone="IMAGE:3945085"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
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Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory,
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Tncyte Genomics, Inc.
Clone distribution: MGC clone distribution information can.be
found through The I.M.A.G.E. Consortium/LLNL at: image.llnl:gov
High quality sequence stop: 688.
                                                                                                    1948
                                                                                                                                                        2008
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 688)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 20-SEP-2000 CDNA clone IMAGE:3945538 5'
                                                                                                     ccagtgccaggaggtcctgcaccacatcagtatgattcctgccaaatgccttcaggaagg
                                                                                                                                                                     -TTGGAAGATTTCAGACCTGTCTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCT
                       241 TCACCCTTTGCTGGTGGTTGCCCCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAA
                                                                           301 CCAGTGCCAGGAGGTCCTGCACCACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGG
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601591442F1 NIH_MGC_7 Homo sapiens
mRNA sequence.
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/clone="IMAGE:3945538"
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insert'size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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hf17h05.x1 Soares_NPL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2932185 3', mRNA sequence.
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Pred. No. 2.1e-264;
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AW572950.1 GI:7237683
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Best Local Similarity 99.8%;
Matches 641; Conservative (
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                                                                                                                                                                                                                                                                      /note="Organ: pooled; Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I:M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

Soares and M. Fatima Bonaldo. "
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco

High quality sequence stop: 459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2850 agtgattccctgcacaccagagacaagcagagtaacaggatcagtgggtctaagtgtccg 2909
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                                                                                                                                                                                                                     /clone="IMAGE:2932185"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                1. 531
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 528; Conservative
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/clone_lib="NIH_MGC_68"
/fissue_type="large_cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dI.
Stet_2: Insert size 1.8 kb. Library constructed by Life
Technologies.
                                                                                                                                                                                                                                                                                                                                                                               Contect: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tissue Probert Strausbergenin. Government: DCTD/DTD/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCMG23 row: k column: 08
High quality sequence stop: 695.
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(Dases 1 to 823)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
(Unpublished (1999)
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BEG19259 823 bp mRNA EST 24-AUG-2000 601473130F1 NIH_MGG_68 Homo sapiens cDNA clone IMAGE:3876223 5
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Best Local Similarity 100.0%; Pred. No. 1e-234;
Matches 465; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:3876223"
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Homo sapiens
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AUTHORS
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                                                                                                                                                                                         AA243700 531 bp mRNA EST 07-MAR-1997 zr68908.s1 Soares.NHRMPLS1 Homo sapiens cDNA clone IMAGE:668606 3' similar to SW:XK50_YEASP P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2_MTD1 INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hillar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston The WashU-Merck Est Project
Uppublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:668606"
/clone_llb="Soares_NhiMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (infc@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -41ml3 fwd. ET from Amersham
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    435 ATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCCACCCTCC 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:5562573"
/db_xref="taxon:9606"
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High quality sequence stop: 466.
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tunic Gene Index
To Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the Info Consortium (info@image.llnl.gov) for further information. Seq primer: -400F from Gibco
High quality sequence stop: 442.
Location/Qualifiers
I. 451
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
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IMAGE:1756895 3' similar to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8
KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                    433
                                                                                                                                         314 CCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTGCGGCC 373
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tttaaaggaaaccgggcttccaaagtgtgtactttctggacctccacaactggaaaata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:1756895"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_statge="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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/clone_"IMAGE:3847226"
/clone_lib="NIH_MGC_65"
/tlssue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORI6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo GT.
Average insert size 1.8 kb. Library constructed by Life
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Fumor Gene Index
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                                                                                                                                                                                                                                                                                                                         AW510825 499 bp mRNA EST 03-MAR-2000 hd40b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2911965 3', mRNA sequence.
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AW510825/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 812)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BEB67512 812 bp mRNA EST 27-SEP-2000 601443010F1 NIH_MGC_65 Homo sapiens CDNA clone IMAGE:3847226 5'BB867512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                             240
                                                                                                                                 259
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0
                                                                 Length 451;
                                                                                                   Indels
                                                                 15.2%; Score 451; DB 17; Lilarity 100.0%; Pred. No. 2.6e-227; Conservative 0; Mismatches 0;
     63
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/db_xref="taxon:9606"
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mRNA sequence.
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Matches 447;
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//note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_GGAP_GGB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-392087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2700 tctatagatgcctcttaggactggtgcctggcacagccgcggggccaggaggctgccacac 2759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2760 ggaagcaagcagatgaactaatttcatttcaaggcagtttttaaagaagtcttggaaaca 2819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2880 agtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtatttcagctgca 2939
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                                                                                                                                                  /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone="IMAGE:2911965"
/clone=11b="Soares_NFL_T_GBC_S1"
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                      High quality sequence stop: 470. Location/Qualifiers
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L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Colone distribution information can be found through the Ling. H.A.G.E. Consortium/Link at: image.linl.gov
Plate: LicMil9 row: o column: 04
High quality sequence stop: 621.
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                                                                                                                                                                                                                       Homo saplens
bisharyota: Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 938)
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BE260626 938 bp mRNA EST 13-JUL-2000 601146116F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161691 5'
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 447; DB 106;
Similarity 100.0%; Pred. No. 3.5e-225;
47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"/db_xref="taxon:9606"
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AUTHORS TITLE JOURNAL

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/Lissue_Lipe_inforcarcinoma cell line"
/Lissue_Lipe="adenocarcinoma cell line"
/Lib_host="DH10B (phage-resistant)"
/Lib_host="Organ: colon; Vector: poTB7; site_1: XhoI; Site_2:
/Lote="Organ: colon; Vector: poTB7; site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size=selected >500pp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
43 a 178 c 161 g 130 t
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 612)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert. Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert. Strausberg@nih.gov

Tissue Procurement: ATCC
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                                                                                                                                                                                                  441 accgggcttccaaagtgtgtactttctggacctccacaactggaaaaatacctcgaagca
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                                                               321 gttcagagactcatgcaggagcacaagttaaaggttgctcgcctggacaacatattcctg
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High quality sequence start: 21
High quality sequence stop: 609.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_15"
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/tissue_type="germinal center B cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausbergenih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. Tissue Procurement: Louis M.
Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: M.C. clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bb.llnl.gov/bbrp/image/image.html
POLYA-NO.
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                                                                                               495 CAGCICCGICCCAGGAGGGAGTGGCAGAGGGAIGCCAITAITACTIGCAAICCIGAGGAA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://www.ncbl.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Fil: (301) 496-1552
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                    AW575677 493 bp mRNA EST. 15-MAR-2000 UI-HF-BMO-ad1-b-07-0-UI.S1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3061957 3', mRNA sequence.
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99.8%; Pred. No. 1.5e-222;
ative 0; Mismatches 1;
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/db_xref="taxon:9606"
                                                                                                                                                               Location/Qualifiers
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AW575677.1 GI:7247216
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I (Dases 1 to 493)

Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Leh.N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-Merck EST Project 1997

Unpublished (1997)

Contact: Wilson RK
WashIngton University School of Medicine
MashIngton University School of Medicine
Tel: 314 286 1810

Fax: 314 286 1810

Exa: 31
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HUMO: NDHOT HOMO SADIAGES CDNA CLONE
tO SW:XK59_YEAST P36159 HYPOTHETICAL 96.8
INTERGENIC REGION: ;, mRNA SEQUENCE.
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Length 612;
                                             Indels
tch 14.8%; Score 438; DB 106; al Similarity 100.0%; Pred. No. 2e-220; 438; Conservative 0; Mismatches 0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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hf45a09.x1 Soares_NTL_T_GBC_S1 Homo sapiens CDNA clone
IMAGE:2934808 3', mRNA sequence.
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/organism="Homo sapiens"
/db_xref="GDB:6019680"
/db_xref="Taxon:9660"
/clone="IMAGE:809862"
/clone_llb="Soares ovary tumor
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                                                                                                                                                                                                        130 g
                                                        /sex="Female"
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AW592601/c
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JOURNAL

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
  IMAGE:1696476 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="DH10B"
                           AI089646.1 GI:3428705
                                                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.4%;
Best Local Similarity 99.6%;
Matches 525; Conservative (
               AI089646
                                                                 ORGANISM
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5.108646/C A1089646 527 bp mRNA EST 18-AUG-1998
7.7FINITION qb16907.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
                                                                   h LLNL; contact the further information.
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                                                                    through LLNL
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through I
IMAGE Consortium (info@image.lln1.gov) for fur
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
                                                                                                                                                                                    /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                14.4%; Score 425; DB 92;
99.8%; Pred. No. 1.5e-213;
tive 0; Mismatches 1;
                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                           /clone="IMAGE:2934808"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Thunor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
High quality sequence stop: 463.
Location/Qualifiers
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Pred. No. 1.5e-213;
0; Mismatches 2; Indels
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/organism="Homo sapiens"
/do_xref="Homo:9606"
/clone="IMAGE:1666476"
/clone_lib="Soares_pregnant_uterus_NDHPU"
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Homo sapiens
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cons. Library Arrayed by: Greg Lennon, Ph.D.

cons. Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-blo.llnl.gov/bbrp/image/image.html
Insert Length: 733 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers
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                                                                                                                                                               tf92g05.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2106776 3' similar to SW:XX59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MID1 INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         fissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BFIGAP), Tumor Gene Index
           Gaps
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                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D.,
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/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
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100.0%; Pred. No. 2e-211;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tell: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                         AI468143.1 GI:4330233
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1 ececcececaagaccecerececaccaecaccaecaagaagaccecaaccereeg

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1...536
/organism="Homo sapiens"
/db_xref="laxon:960e"
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/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
oligo-dr track not found. Not I site shown in beginning of sequence
is likely interpal to the message. cDNA Library Preparation: M.B.
Soares Lab Coine distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 536)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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UI-H-BII-afx-f-12-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2723471 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GACACGAATGCACTGGTCTAATGTTGGGGGCTTAAGTGGAATGATTCTTACTTTAAAGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 gggegecgegetetaegtetteteegagtteaaceggtatetetteaactgtggagaagg
                                                                                                                                                                                                                                320 ogttcagagactcatgcaggagcacaagttaaaggttgctcgcctggacaacatattcct
                                                                                                                                                                                                                                                                                            380 gacacgaatgcactggtctaatgttgggggcttaagtggaatgattcttactttaaagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GGGCGCCGCCTCTACGTCTTCTCCGAGTTCAACCGGTATCTCTTCAACTGTGGAAGG
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Unpublished (1997)
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AW304130.1 GI:6713819

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NCI_CGAP_Lu19, NCI_CGAP_GC6,

NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,

Single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI_CGAP_Kid3 pool 1 LiAM 334-337, 3862-3863,

NCI_CGAP_Kid3 pool 1 LiAM 334-337, 1456088-1456775, 1500552-150285); NCI_CGAP_Kid5 pool 1 LiAM 338-3342, 376-3785, 376-3786 [IMAGE CloneIDS 1323912-132581, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LiAM 3575-3582, 3851-3854 [IMAGE CloneIDS 127096-128631, 1520904-1522439); NCI_CGAP_GC4 pool 1 LiAM 3164-3167, 3716-3720, 373-3735 [IMAGE CloneIDS 127096-128631, 1469064-1470983, 1475592-1476743); NCI_CGAP_FC2 pool 1 LiAM 2457-2459, 2758-2759, 3062-3068 [IMAGE CloneIDS 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_CO10 pool 1 LiAM 2644-1145351). Subtraction was performed as previously described [Bonaldo, Lenono & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 acacgaatgcactggtctaatgttgggggcttaagtggaatgattcttactttaaaggaa 440
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Pred. No. 2e-211;
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TAG_TISSUE=lung
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143 c
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Best Local Similarity 99.8%;
Matches 471; Conservative
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AW304130 404 bp mRNA EST 18-JAN-2000 xs13e05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2769536 3' similar to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-WYD1 INTERGENIC REGION. ;, mRNA sequence.

X304130 SFINITION

CESSION

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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
Email: Robert_Strausberg@inh.gov
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Lorary Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Kidney; Vector: pr773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site_2: ECO RI: Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-133391, 1456007-1456775, and Fatima Bonaldo. "Subtraction by Bento Soares and M. Fatima Bonaldo."
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                                                                               Eukaryota
Eukaryota
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 404)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1. .404
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Unpublished (1997)
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1 (bases 1 to 474)
1 (lases 1 to 474)
1 (lases 1 to 474)
1 (kases 1 to 474)
1 (kases 1 to 474)
1 (kacaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie 7, T., Matcrston, R. and Wilson, R.
Washu-Marck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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/lab_host="PHIOB (ampicillin resistant)"
/lab_host="THIOB (ampicillin resistant)"
/lab_host="THIOB (ampicillin resistant)"
/lab_host="Thiob (ampicillin resistant)"
/lab_host="Thiob (ampicillin resistant)"
/lab_host="In resistant"
/lab_host="In resistant"
/lab (ampicillin resistant)
/lab (ampicillin resistant
                                                                                                                                                                                                                                                                                  tumor NbHOT Homo sapiens cDNA clone
to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8
INTERGENIC REGION: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 465.
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301 TACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTC 360
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                /clone_lib="Soares ovary tumor NbHOT"
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100.0%; Pred. No. 2.3e-201;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
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120 c 129 g
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                                                                                                                                                                                                                                                                                                                                                                                                    AA291670.1 GI:1939648
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='Indage:1838237"
/clone='Indage:1838237"
/clone='Indage:1838237"
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/db_host='BH10B (phage=resistent)
/nb_host='BH10B (phage=resistent)
/note='Organ: ovary: vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size=selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: DCTPDTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM524 row: 1 column: 14
High quality sequence stop: 781.
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                                       ccactctgccccagaatacgaggatgaaaccatgacagtttaccagatccccatacacag
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 992)
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Pred. No. 2.8e-200;
); Mismatches 1;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 574)
1 (hases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM52 row: n column: 14
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1672 ctgtgtttgtgtcccacctgcacgcagatcac 1703
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Taxon:2560077"
/clone=lib="NIH_MGC_17"
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Exaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

2. 1 (bases 1 to 431)

8. Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A., Bult

8. (C.J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocapne, J. D., White

9. (Sutton, G., Blake, J. A., Brandon, R. C., Man-Wai, C., Clayton, R. A.,

Cline, T. R., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Fitzgerald

9. L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A.,

6. Ghehm, C. L., Hannan, M. C., Hedblom, E., Hikle, P. S., Tr., Kelley, J. M.,

8. Kelley, J. C., Liu, L. -I., Marmaros, S. M., Merrick, J. M., Shirley, R.,

Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R.,

8. Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y.,
/tissue_type="rhabdomyosarcoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; CoNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCACGAG(G). Size-selected >500pp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

19 c 167 g 119 t 6 others
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5' end, mRNA sequence.
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Pred. No. 8.2e-192;
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Best Local Similarity 99.8%;
Matches 434; Conservative
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Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dünke, D., Ferrie, A., Fischer, C., Hastlings, G.A., He, W.W.
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kimi, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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                                                                                                                                                                                              Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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The Institute for Genomic
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                                                                                                                                                                                                                                                                                                              Other_ESTs: THC175624
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/tissue_type" adenocarcinoma cell line"
/lab_host="nullOB (phage-resistant)"
/lab_host="nullOB (phage-resistant)"
/note="organ: ovary; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dr priming. Directionally
Cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >50bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis Xit
(Stratagene) and Superscript II RT (Life Technologies)."
25 a 263 c 281 g 179 t I others
                                                                                                                                                                                                                                         Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenth.gov
Tissue Procurement: DCTD/PDF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The T.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM524 row: g column: 18
High quality sequence stop: 668.
Location/Qualifiers
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                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 949)
NHH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BE744197 949 bp mRNA EST 15-SEP-2000 601577168F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838121 5'
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Pred. No. 5.7e-186;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3838121"
/clone_lib="NIH_MGC_9"
                                                                                                                         BE744197.1 GI:10158189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.68;
99.78;
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Matches 613; Conservative
                                                              mRNA sequence.
BE744197
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KEYWORDS
SOURCE
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BE900936
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/clone_lib="NIH AGC_71"
/clone_lib="NIH AGC_71"
/tissue_trpe="lelomyosarcoma"
/lab_host="Organ: utefus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. " 100 c 106 g 70 t
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                                                                                                                                                                                       BE883616 370 bp mRNA EST 27-SEP-2000
601508091F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909527 5'
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
299 CACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTGGTTCACATGGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                    cacccagcacttggtcctgaatgagaactgtgcctcagttcacaaccttcgcagcacaa
                                                                                                           419 CACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTTCGCAGCCACAA
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/db_xref="taxon:9606"
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Location/Qualifiers
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/iissue_type="forticarcinoma"
/lab_host="DH10B (phage-resistant)"
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/nab_host="DH10B (phage-resistant)"
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/nabe="Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGcAGGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cbNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 206 c 215 g 159 t
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NIH-WGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM834 row: k column: 01
                                                                                                                   2211
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                                                                                                                240
                               BE900936 745 bp mRNA EST 29-SEP-2000 601674206F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:3957240 9
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                                                                                                                                                                                                                                                                                                  181 TGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGCG
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/clone_lib="NIH_MGC_21"
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., R., Williamson,A., Wohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R87541 518 bp mRNA EST 16-AUG-1995 ym89b04.rl Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:166063 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
Insert Size: 2215
High quality sequence stops: 331 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2215 Std Error: 0.00
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                                      Gaps
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                                                                                                                                                                                                                                                                                                 1918 gattgatcagttcgctgttgcgaacatgtgatttggaagagtttcagacctgtctggtgc
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Length 745;
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Query Match 12.4%; Score 368; DB 137; Best Local Similarity 100.0%; Pred. No. 2.5e-183; Matches 368; Conservative 0; Mismatches 0;
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High quality sequence stop: 331.
Location/Qualifiers
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28h1 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
, mRNA sequence.
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ORGANISM.-Homo sapiens
ORGANISM.-Homo sapiens
ORGANISM.-Homo sapiens
EDRATYOUS, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
EPERENCE 1 (bases 1 to 855)
AUTHORS Macke, J., Smallwood, P. and Nathans, J.
IIILE Adult Human Retina CDNA
JOORNAL Unpublished (1996)
OWMENT CONTACT: Dr. Jeremy Nathans
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Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
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100.0%; Pred. No. 7.3e-175;
ive 0; Mismatches 0;
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1. 790

// Organism="Homo sapiens"

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/note="Organ: skin; Vector: pCWV-SPORT6; Site_1: Not1:

// Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.

Pechnologies."
Technologies.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. 3.4e-172;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                             60
                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                          Plate: LLCM739 row: 1 column:
High quality sequence stop: 662.
Location/Qualifiers
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AA811170.1 GI:2880781
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                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases-1 to 790)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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rel: 410 955 4678
Fax: 410 614 0827
Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
PCR PRIMERS
FORWARD: CTTTGGAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTCTTCCAGGGTAA
Seq primer: GGGTAAAAAGCAAAAAAAATT.
                                                                                                                                                                                                                                           Location/Qualifiers
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446 bp mRNA EST 21-0CT-1997
aB277h02.r1 Stratagene lung (#937210) Homo saptiens CDNA clone
IMAGE:842067 5' Similar to SW:KK59_YEAST P36159 HYPOTHETICAL
KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION. ; mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/sex="male"
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/db_xref="taxon:9606"
/clone="IMAGE:842067"
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                                                                                                                                  David Allman,
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Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Seq

Clone distribution: NCI-CGAP clone distribution inf

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 885 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 377.
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Aorganism-"Homo sapiens"
(db.xref="taxon:9606"
Clone="IMAGE:1334020"
Clone="ID="NCI_GGAP_GCB1"
(tissue_type="germinal center B cell"
(lab_host="DH108"
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Best Local Similarity 100.0%; Pred. No. 4.2e-170;
Matches 343; Conservative 0; Mismatches 0;
                   Unpublished (1997)
Contract: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Hillier, D., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Walte, Y., Walte, T., Waterston, R. and Wilson, R., Theising, B., Unpublished (1997)
                                          AA679618 452 bp mRNA EST 02-DEC-1997 37202.2 I Gesler Wilms tumor Homo sapians DNA clone IMAGE:1128502 3' similar to SN:YK59 YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MIDI INTERGENIC REGION.; mRNA sequence.
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Gessler Wilms tumor"
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/lab_host="DH108"
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JOMMENT
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DESULT 3:
                                                                                                                                      CCESSION
                                                                                                                                                           TERSION TEYWORDS
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/lob_lost="DHIOB (phage-resistant)"
//note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: BcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAGGGG. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 698) NIH-MGC http://www.nobi.nlm.nih.gov/MGC/.
NIH-MGC http://www.nobi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM807 row: f column: 23

High quality sequence stop: 389.

Location/Oualiflers

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BE795434 698 bp mRNA EST 20-SEP-2000 601592991F1 NIH_MGC_7 Homo sapiens CDNA clone IMAGE:3946774 5'
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                                                                                                      octogaagcaatcaaaatattttctggtccattgaaaggaatagaactggctgtgcggcc
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Best Local Similarity 99.7%; Pred. No. 5e-169;
Matches 391; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism~"Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:3946774"
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/fissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                            ccactctgccccagaatacgaggatgaaaccatgacagttta 592
                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BE795434
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/tissue_type="adenocarcinoma cell line"
/lab_host="DHIOB (phage-resistanty"
/lab_host="DHIOB (phage-resistanty"
/note="Corgan: ovary: Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGGG. size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Tel: (301) 496-1550

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Theyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through The I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence stop: 672.
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345 AAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGGTATGGAGCTGTGCCGAGGCTT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601574609F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835658 5' MRNA secure content of the conten
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                                                                                             gggctcccacataagcactagtctatagatgcctcttaggactggtgcctggcacagccg
                                                                                                                                              285 GGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCCTGGCACAGCCG
                                                                                                                                                                                                                                                                                       cgggccaggaggctgccacacggaagcaagcagatgaactaatttcatttcaaggcagtt
                                                                                                                                                                                                                                                                                                                              225 CGGCCAGGAGGCTGCCACACGGAAGCAGATGAACTAATTTCATTTCAAGGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2799 tttaaaagaagtettggaaacagaeggeggeaeettteetetaateeageaaagtgattee
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Pred. No. 2.6e-165;
0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:3835658"
/clone=lib="NIH_MGC_9"
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99.8%;
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BE742908
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TITLE
JOURNAL
                                                                                             2679
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KEYWORDS
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/note="Vector: pT779-Pac; Site_1: NotI;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 345)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                         gggcttgccaagtatcttgctgcagagagaacgcgccttggcatctttgggaaagccgct 1768
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: M.G. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    241 TCACCCTTTGCTGGTGGTTGCCCCCAACCAGGTCAAAGCCTGGCTCCAGGAGTACCACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 CCAGTGCCAGGAGGTCCTGCACCACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGG
                                                                                                                                                                                               GGGCTTGCCAAGTATCTTGCTGCAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCT
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11 Similarity 100.0%; Pred. No. 1.9e-167;
338; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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COURCE

REFERENCE AUTHORS TITLE JOURNAL

OMMENT

EATURES

CCESSION FERSION SEXWORDS

NOITINITE RESULT 37 3W407520/c

Euteleostom1;

Gaps

Indels

Best Local Similarity 99.8 Matches 454; Conservative

Local

Matches 2619

SASE COUNT

Length 677;

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/note="Organ: muscle: Vector: poTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 416)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: ACC constitution: Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM85 row: f column: 12
High quality Sequence stop: 416.
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2217 aaccacttcagccagcgctatgccaaggtcccctcttcagccccaacttcagcgagaaa
                                                                                                         AGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGTCTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.aov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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TITLE
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for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at: image.llnl.gov
Plate: LLCM/754 row: d column: 11
High quality sequence stop: 631.
Location/Qualifiers
I 940
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 940)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.3e-163;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone="IMAGE:3926362"
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99.7%;
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Best Local Similarity 99.7°
Matches 380; Conservative
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BE743831
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AUTHORS
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COMMENT
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KEYWORDS
SOURCE
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BE743831
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np66h03.sl NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1131317 3' similar to SW:XK59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MT1 INTERGENIC REGION, ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 AAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCGCCCTTTCCTCTAATCCAGCAA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2790 aaggcagtttttaaagaagtcttggaaacagacggcgcacctttcctctaatccagcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2910 agacttaacgaaaatagtatttcagctgcaataaagattgagtttgcaa 2958
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Pred. No. 1.5e-160;
0; Mismatches 4;
   www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1291 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 467.
Location/Qualifiers
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al Similarity 99.2%;
525; Conservative
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/tibsue_type="adenocarcinoma cell line"
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/note="Core" bH10B (phage=resistant)"
/note="Core" bH10B (phage=resistant)"
/note="Core" bh10B (phage=resistant)"
/note="Core" bh10B (phage=resistant)
/note="Core" by oligo-dT priming. Directionally
/cloned into EcoRI/Ahol sites using the following 5'
adaptor: GGCACAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
50 a 242 c 281 g 167 t
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Na Sequencing By: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M. G.B. Consortium/LLNL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 511)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/PRGAP), Tumor Gen Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gctgtgtactcctccagatcctggtgctgcttttgtggtggtagaatgtccagatgaaag 994
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                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                           Ouery Match 11.1%; Score 329; DB 135; Best Local Similarity 100.0%; Pred. No. 1.2e-162; Matches 329; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mŘNA sequence.
A1937465
A1937465.1 GI:5676335
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                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Tel: (301) 496-1550

Tel: (301) 496-1550

Tissue Probert Strausbergenih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NGI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 40m13 fwd. ET from Amersham

High quality sequence stop: 383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I ollgo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NCI_CGAP_BI1.1. Library was constructed by Bento Soares and M. Fatina Bonaldo.
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 397)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1131317"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .397
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100 c 111 g
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   GI:255532
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Unpublished (1997)
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0.7 a 139 c 131 g 102 t 3 others
   R55841 482 bp mRNA EST 23-MAY-1995 yg890d1.r1 Soares infant brain INIB Homo saptiens cDNA clone IMAGE:40931 5' similar to SP:XKS2_XEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC ; mRNA sequence.
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1 (bases 1 to 482)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-wark Est Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 1777
Hish quality sequence stops: 387 Source: IMAGE Consortium, LLNL
Hish clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1777 Std Error: 0.00
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23-MAY-1995
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ilarity 100.0%; Pred. No. 1.7e-159;
Conservative 0; Mismatches 0;
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Location/Qualifiers
                                                                                                                                                            R55841.1 GI:825947
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/tissue_type="choriocarcinoma"
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/note="norgan: placenta; vector: poTB7; Site_1: XhoI;
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Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: AFCE
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCN841 row: j column: 23
High quality Sequence stop: 732.
Location/Qualifiers
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 735)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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601677393F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:3959926 {
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/lab_host="DH1T3B"
/lab_host="DH1T3B"
/lab_host="DH10B"
/lab_host="DH1T3B"
/lab_ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 366)

1 (lases I to 366)

1 (lases I to 366)

M., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

Unpublished (1995)
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AA233087
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 346.
Location/Qualifiers
                                                                                                                                                                                                                                                         1670 tgctgtgtttgtgtcccacctgcacgcagatcaccacacgggcttgccaagtatcttgct 1729
                                                                                                                                                                                                                                                                                                      163 TGCCACACTTGTCAACATAAGCCCCGACACGTCTGCTACTGGACTGTGGTGAGGGGCAC 222
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Matches 365; Conservative
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PEFERENCE AUTHORS

TITLE JOURNAL JAMENT

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Bunmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 491)

I (bases 1 to 491)

I (bases 1 to 491)

Krizman, D., Rucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

In published (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1800
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pr7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. lst strand cDNA was primed
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lange.llnl.gov) for further information.
Seq primer: -4(0nl3 fwd. ET from Amersham.
Location/Qualifiers
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                                                                                                             1372 gcaatcctgaggaattcatagttgaggcgctgcagcttcccaacttccagcagagcgtgc 1431
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/organism="Homo sapiens"
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/db_armelib="IMAGE:459985"
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0
                                            Length 735;
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                                              Score 307; DB 137;
Pred. No. 5.2e-151;
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                                  10.4%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 480)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,T.R., Williamson,A., Wohldman,P. and Wilson,R.
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R90875 480 bp mRNA EST 25-AUG-1995 ynOld02.rl Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167139 5', mRNA sequence.
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                                                                                                                                                                                          Length 491;
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                                                                                                                                                                                        10.2%; Score 302; DB 10;
larity 99.3%; Pred. No. 2.3e-148;
Conservative 0; Mismatches 3;
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Contact: Wilson RK
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;, mRNA sequence.

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        High quality sequence stops: 263 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 4441 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 263.
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/clone="IXAGE:167139"
/clone="lb="Soares adult brain N2b4HB55x"
/sex="Male"
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/organism="Homo sapiens"
/db_xref="GDB:587834"
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Wallond Cancer Index
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
Info@image.llnl.gov
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity not found
Seq primer: -40UP from Gibco
High quality sequence stop: 494.
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/db_xref="taxon:9606"
/db_xref="Taxon:9606"
/clone="InAGE:303219"
/clone=lib="NoI_CGAP_Kid11"
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/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 511)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Best Local Similarity 99.6%; Pred. No. 7.7e-148;
Matches 471; Conservative 0; Mismatches 1; Indels 1; Gaps
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AW771657 511 bp mRNA EST 04-MAY-2000 hn59h06.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032219 similar to SW:XK59_XEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN

SFINITION

48

RESULT 4
AW771657
LOCUS

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7 TAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCCACATTTGGGCAGCTGTGCC
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AUTHORS
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-BN0036-260
400-015-e06&ft3=2000-04-26&t4=1)
Seq primer: puc.18 forward
High quality sequence start: 9
High quality sequence stop: 297.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 297)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagali, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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S23-BN00386-260400-015-e06 BN0036 Homo sapiens cDNA, mRNA sequence.
AW994476 GI:8254699
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
ggetgtgcggccccactctgccccagaatacgaggatgaaaccatgacagtttaccagat 598
                                                                                                            399 GGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTTTACCAGAT
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                                                                                                                                                                                            459 CCCCATACACAGTGAACAGAGGGGGAAAGCACCAACCATGGCAGAGTCCAG 511
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20202663
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93 c 82 g 62 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0036"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
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taageceegaeaegtetetgetaetggaetgtggtgagggeaeatttgggeagetgtgee 1626

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/note="Vector: pspor1; Site_1: Sal1; Site_2: Not1; RNA was prepared from a pool of 6 anonymous Wilms' tumor RNAs. RNA was prepared by acid-phenol, followed by one round of oligo dr selection. CDNA library preparation was with the BRL/Life Tech. Superscript Plasmid system. An oligo-dr Not1 primer for first strand synthesis generated geggecoc(t) at the 3' end of the clones. A 5' Sal1 adaptor was used with sequence 5'-gtogaccoagegtcog-a was used with sequence 5'-gtogaccoagegtcog-selecting cDNAs were size selected (average size 2 kb), Not1 digested, and ligated into Not1/Sal1-cut pSPORT1. Library was constructed by Dr. Manfred Gessler."
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: esclewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity on wrong strand
Fossible reversed clone: polyT not found
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 391.
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1 (bases 1 to 404)
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A142605.51 Gessler Wilms tumor Homo sapiens CDNA clone
IMAGE:1701344 3' similar to SW:YKF9_YEBST P36159 HYPOTHETICAL 96.8
KD PROTEIN IN SIS2-MIDI INTERGENIC REGION. ; mRNA sequence.
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/clone_lib="Gessler Wilms tumor"
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/lab_host="DH10B"
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Email: jmargolin@txccc.org
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7g2la09.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3307096 3',
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can I found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 493.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                   114 GACTCGGGCGCGCGCTCTACGTCTTCTCCGAGTTCAACCGGTATCTCTTCAACTGTGGA 173
                                                                                                                          gaaggcgttcagagactcatgcaggagcacaagttaaaggttgctcgcctggacaacata 374
                                                                                                                                                                               ttoctgacacgaatgcactggtctaatgttgggggcttaagtggaatgattcttacttta 434
                                         Gaps
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              Length 404;
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/db_xref="taxon:9606"
/clone="Ixacon:9606"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="qlioblastoma (pooled)"
/lab_host="DH108"
          9.8%; Score 291; 25.142;
100.0%; Pred. No. 1.5e-142;
tive 0; Mismatches 0;
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           Query Match
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Matches 291; Conservative
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Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.
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"Contract: Dr. Judith F. Margolin
Human Genome Sequencing Center at Baylor College of Medicine and
Texas Children's Cancer Center
                                                                                                                                                                                                                                                                                                                                                                         2702
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                                                                                                                                                                                                          agcaagcagatgaactaatttcatttcaaggcagtttttaaagaagtctttggaaacagac 2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2823 ggcggcacctttcctctaatccagcaaagtgattccctgcacaccagagacaagcagagt 2882
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atagatgcctcttaggactggtgcctggcacagccgcggggccaggaggctgccacacgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 GGGGGCACCTTTCCTCTAATCCAGCAAATGATTCCCTGCACACACGAGACAAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens •
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 414)
• Wel,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project
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                                                                                                                                                                   ö
                                                                                                                            Length 494;
normalized, and was constructed M.Fatima Bonaldo." 124 g 135 t
                                                                                                                                                                   Indels
                                                                                                                        Score 290; DB 136;
Pred. No. 5.2e-142;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  One Baylor Plaza, Houston, TX 77030, USA Tel: 713 770 4536
Fax: 713 770 4038
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Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melssner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,W.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
                                                                                                                                                                                                                                                                          Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: Mi3 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W37486 397 bp mRNA EST 10-OCT-1996 COCGO STORES SOURCES PARACHYSCIAL LUMOR_NDHPA HOMO SADIENS CONE LIMAGE:321917 3' SIMILAT tO SW:YK59_KBST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION. [1]; , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1043 aaaggcagatgccccgtggccttggtggttcacatggccccagcatctgtgcttgtgga 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1103 cagcaggtaccagcagtggatggagaggtttgggcctgacacccagcacttggtcctgaa 1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CAGCAGGTACCAGCAGTGGATGGAGGTTTGGGCCTGACACCCCAGCACTTGGTCCTGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 others
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Pred. No. 6.7e-140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="ATCC (inhost):153799"
/db_xref="taxon:9606"
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="T-lymphocyte"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTs: THC175624
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W37486.1 GI:1319080
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DEFINITION
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VERSION
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, M.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Handa, M.C., Heddlom, E.L., Hinkle, P.S.JT., Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggcacctgcgcacgcgagagaagcgcggaccgtcggggtgctccggcggcgcccaaacaccg 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 agggacgcaccatatcgcaggcacccgccgccgcggggggcggcgaggacccgctgc 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 GGCACCTGCGCACGCGAGAGAGCGCGGGACCGTCGGGGTGCTCCGGCGGCGCCCAAACACCC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 TGTACCTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCGCTCTACGTCTTCT 307
                                                                                                                                                                   acute lymphoblastic
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EST61719 Activated T-cells XX Homo sapiens CDNA 5' end, mRNA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 9.7%; Score 287; DB 105; Length 414; Local Similarity 100.0%; Pred. No. 2e-140; nes 287; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukemia Baylor-HGSC project=TCBA"
                                                                                                                                                                   cell
                                                                                                                                                                                                                                                          /tissue_type="leukopheresis"
/cell_type="pere B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH109"
                                                                                                                                   /clone="TCBAP1522"
/clone_lib="Pediatric pre-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 t
                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
            .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 g
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AA353573.1 GI:2005893
EST.
                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 c
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-25UK
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352 CTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAA 396
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99.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .394
                                                                                                                                mRNA sequence.
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Best Local Similarity
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                                                                                                                                                   AW248468
                                                                                                                                                                                                           nman.
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                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                      RESULT 55
AW248468/c
LOCUS
                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                 REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:321917"
/clone=lib="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Yogan: parathyroid gland; Vector: pT7T3D (Pharmacia with a modified polylinker; Site_1: Not I; Site_2: Eco RI; ist strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTT-3'], double-stranded cDNA was size selected, ligated to EC RI adapters (Pharmacia), digested with Not I and cloned into the Not I and EC RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                               Bukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 397)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikhin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Wailliamson,A., Wohldmann,P. and Wilson,R.

The WashU-warck EST Project
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: similarity on wrong strand Insert Length: 678 Std Error: 0.00
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                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.6%; Score 285; DB 146;
llarity 100.0%; Pred. No. 2.3e-139;
Conservative 0; Mismatches 0;
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    .397
    /organism="Homo sapiens"
    /db_xref="GDB:1259575"
    /db_xref="taxon:9606"

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                                                                       EFERENCE
                                                                                         AUTHORS
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Actional institutes of nearin, manumatian dene contection (Mac.) other_ESTS: 2820640.5prime
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (Linu) DNA Sequencing by: Berkeley MGC Sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/Lila at:
www-bio.linl.gov/bbrp/image/himage.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross_match from University of Rashingtion Genome Center.
PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
ptrp://www.genome.washington.edu Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
polyadenylated.
AW248468 394 bp mRNA EST 07-JAN-2000
2820640.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820640 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: lung; Vector: pore; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2573 gcccacgcacgcaccgtatctgcctccttgctggtagaagctgaagagcacggtcc 2532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 CCAGGAGGCAGCTCAGGATAGGTGGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAA 275
                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:2820640"
/clone_lib="NHIMGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DHIOB (phage-resistant)"
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Pred. No. 7.7e-139;
); Mismatches 2;
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High quality sequence stop: 213.
Location/Qualifiers
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T34216
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 489)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1275 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 446.
Location/Qualifiers
1. 489
                                                                                                                                                                                                                                                              AI803400 489 bp mRNA EST 13-DEC-1999 tc42f03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2067293 3', mRNA sequence.
                                                                                  2872
                                                                                                                                2873 caagcagagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtatttc 2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
                                                                                                                                                      94 CAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTC 35
                                                214 GCCACACGGAAGCAAGCAGATGAACTAATTTCATTTCAAGGCAGTTTTAAAAGAAGTCAT
                                                                                2813 ggaaacagacggcacctttcctctaatccagcaaagtgattccctgcacaccagaga
                                                                                             gccacacggaagcaagcagatgaactaatttcatttcaaggcagtttttaaagaagtctt
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Pred. No. 2.6e-138;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2067293"
                                                                                                                                                                              AI803400.1 GI:5368962
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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 307)

Sadams, D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

C.J., Lee, N., Kirkness, E.F., Warnatock, K.G., Gocayne, J.D., White

C.J., Lee, N., Kirkness, E.F., Warnadon, R.C., Chiu, M.W., Glayton, R.A.,

Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald

L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S. M., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Harkled, P.S., Kelley, J.M.,

Klimek, K.M., Kelley, J.C., Liu, L.I., Maymaros, S.M., Merick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pellegrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weilman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J.,

Kunsch, C., Ji, H., Melssner, P.S., Olsen, H., Raymond, L.,

Kunsch, C., Ji, H., Li, H., Melssner, P.S., Olsen, H., Raymond, L.,

W.R.F., Wang, J., Ward, C., Yu, G. L., Ruben, S.M., Dillon, P.J., Fannon

W. P.F., Wing, J., Ward, C., Yu, G. L., Ruben, S.M., Dillon, P.J., Fannon

W. P. F., Wing, J., Ward, C., Yu, G. L., Ruben, S.M., Dillon, P.J., Fannon

W. P. F., Wang, J., Ward, C., Yu, G., L., Ruben, S.M., Dillon, P.J., Fannon

W. P. F., Wang, J., Ward, C., Yu, G., L., Ruben, S.M., Dillon, P.J., Fannon

W. P. F., Wang, J., Ward, C., Yu, G., L., Ruben, S.M., Dillon, P.J., Fannon

W. P. F., Wang, J., Ward, C., Yu, G., L., Ruben, S.M., Dillon, P.J., Fannon

W. P. F., Wang, J., Ward, C., Yu, G., L., Ruben, S.M., Dillon, P.J., Fannon

W. P. F., Wang, J., Ward, Fields, C., Fraser, C. M., and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T34216 307 bp mRNA EST 06-SEP-1995
EST64346 Human White blood cells Homo sapiens cDNA 5' end similar
to None, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 AGGIGGIAIGGAGCIGIGCCGAGGCIIGGGGICCCACAIAAGCACIAGICIAIAGAIGCC
                                                                                                                                                           932 Clopper Rd, Gaithersburg, MD 20878
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: THC15444
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/note="Vector: pr773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was prepared from I2 pooled bulk tumor samples and primed with a Not I - Oilgo(dT) primer. Double-stranded cDNA was Ilgated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2834 teetetaateeageaaagtgatteeetgeacaceagagacaageagagtaaeaggateag 2893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 GIGGTATGGAGCTGTGCCGAGGCTTGGGGTCCCACATAAGCACTAGTCTATAGATGCCTC 245
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ILO-ST0002-160599-003 ST0002 Homo sapiens CDNA, mRNA sequence.
AW806551
AW806551.1 GI:7899550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2654 gtggtatggagctgtgccgaggcttgggctcccacataagcactagtctatagatgcctc
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 336.
Location/Qualifiers
                                                                                                                /clone="IMAGE:925867"
/clone_lib="NCI_CGAP_Co3"
                                                                          /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                      /tissue_type="colon"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                                  normalization.
135 c 1
                                                                                                                                                        /sex="pooled"
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information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
                                                        For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfoetdb.tigr.org) Seq primer: Mi3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1855 tcagtatgattcctgccaaatgccttcaggaaggggctgagatctccagtcctgcagtgg 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                              1735 gagaaacgcgccttggcatctttgggaaagccgcttcaccctttgctggtggttgcccca 1794
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Homo sapiens cDNA clone IMAGE:925867
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                                                                                                                                                                                                                                                                                                                                                                  Length 307;
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 680 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Bento Soares, Ph.D.
                                                                                                                                            1. .307
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="ARCC (inhost):104947"
/db_xref="taxon:9606"
/clone_lib="Human White blood cells"
/tissue_type="white blood cells"
/note="Organ: blood"
81 c 86 g 75 t
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                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 282; DB 145;
100.0%; Pred. No. 8.7e-138;
tive 0; Mismatches 0;
                                                                                                                                    Location/Qualifiers
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
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nf76f10.s1 NCI_CGAP_Co3
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 282; Conservative
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AA534478
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Matches 326; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=LLO-ST0002-160
599-003&t1=-1999-05-16&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 278.
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 278)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products sterived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Breat and Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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ab48b06.rl Stratagene lung carcinoma 937218 Homo sapiens CDNA clone
Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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20202663
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84 c 70 g 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0002"
/dev_stgge="Adult"
                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                   Simpson, A.J.
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Matches 276; Conserv
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E l'Asservations (Craniata; Vertebrata; Buteleostomi; Butarota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 'to 461)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

Washu-Rot human EST Project
Uppublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                     gh LLNL; contact the further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_InAGE:844019"
/clone_lib="Strategene lung carcinoma 937218"
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/cell_line="NCI-H69"
                                                                                                                                                                                                                                                                                                                                                                                           Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (infoéimage.llnl.gov) for further
INAGE Length: 694 Std Error: 0.00
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 453.
Location/Qualifiers
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99.7%; Pred. No. 1.3e-134;
tive 0; Mismatches 1;
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/db_xref="taxon:9606"
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             AA994126
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dlone_lib="Br0041"
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/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVO&t2=QVO-BTOO41-03099-013-e09413=1999-09-03644=1)
Seq primer: puc 18 forward High quality sequence start: 75
High quality sequence stop: 364.
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                                               NA EST 16-NOV-1999
BT0041 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 364)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1205 tcaaacccagctcaacctcatccaccggacatcttccccctgctcaccagtttccgctg 1264
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                                             AW175581 364 bp mRNA
QVO-BT0041-030999-013-e09 BT0
                                                                             AW175581
AW175581.1 GI:6441618
                                                                                                                                                                                                                                                                                                                                      rel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
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Best Local S
Matches 274
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/ncce="Organ" Displayed; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHil9W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Scares and M. Fatima Bonaldo. "

119 c 1127 g 96 t
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AA994126 457 bp mRNA EST 27-AUG-1998
0308066.31 SOARES-NFL_GEC_S1 HOMO SAPLENS CDNA CLONE
IMAGE:1628531 3' similar to SW:XK59 YEAST P36159 HYPOTHEDICAL 96.8
KD PROTEIN IN SIS2-WID1 INTERGENIC REGION.; mRNA SEQUENCE.
                                                                                                                                                                                                                 Homomore appiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Email: Robert_Strausbergenih.gov
This clone is available royally-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1193 Std Error: 0.00
Seq primer: -40m13 fwd. Err from Amersham
High quality sequence stop: 439.
Location/Qualiflers.
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100.0%; Pred. No. 5.2e-133;
Live 0; Mismatches 0;
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AA994126.1 GI:3180671
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//issue_type="adenocarcinoma cell line"
//ib. host="DHIOB (phage-resistant)"
//ib. host="DHIOB (phage-resistant)"
//ib. host="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGGG, size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-cDNA synthesis kit
(Strategene) and Superscript II RT (Life Technologies)."
259 c 316 g 182 t
                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM522 row. o column: 06
High quality sequence stop: 726.
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                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 984 N.M. M.M. MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                            BE744876 984 bp mRNA EST 15-SEP-2000 601576324F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3837533 5'
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Pred. No. 2.8e-129;
0; Mismatches 1; Indels 1;
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/clone_lib="NIH_MGC_9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                BE744876.1 GI:10158868
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Best Local Similarity 99.5%;
Matches 436; Conservative
                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                        mRNA sequence.
                                                                                                                                                                                                Homo sapiens
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    ESULT 6:3744876
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 773 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 368.
Location/Qualifiers
AI033108 410 bp mRNA EST 28-AUG-1998 ow98908.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens CDNA clone IMAGE:1654910 3', mRNA sequence.
                                                                            1326 cagctccgtcccaggaggagtggcagagggatgccattattacttgcaatcctgaggaa 1385
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                                                                                                                  603 CAGCTCCGTCCCAGGAGGGAGTGGCAGAGGGATGCCATTATTACTTGCAATCCTGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .410
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/sex="male"
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99.3%; Pred. No. 1.8e-123;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                 AI033108.1 GI:3254061
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405; Conserve
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COMMENT
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Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 479)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G.; Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,

Wath,C.Y., Wylie,T., Waterston,R. and Wilson,R.

Unpublished (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL, contact the
IMAGE Consortium (info@image.linl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 462.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 TGCACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA716607 479 bp mRNA EST 29-DEC-1997 2g68g07.sl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398556 3', mRNA sequence.
                                                                                                                                       2740 gggccaggaggctgccacacggaagcaagcagatgaactaatttcatttcaaggcagtt
                                                                                                                                                                                                                                                                                                                                                             2800 ttaaagaagtettggaaacagacggeggcacettteetetaatecagcaaagtgatteee
                                                                                                                                                                                                                                                                                                                                                                            2860 tgcacaccagagacaagcagagtaacaggatcagtgggtctaagtgtccgagacttaacg
                401 CTGTGTGTGTTCTGCCCCACGCACGCACCCGTATCTGCCCTTGCTGGTAGAAGCTGA
                                                                                                                                                                                                                2680 ggctcccacataagcactagtctatagatgcctcttaggactggtgcctggcacagccgc
                                                                                                                                                                                                                                 281 GGGTCCCACATAAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCCTGGCACAGCTGC
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/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:1306379"
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AA716607/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco High quality sequence stop: 450.
                                                                                                                                                            2851 gtgattccctgcacaccagagacaagcagagtaacaggatcagtgggtctaagtgtccga 2910
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 AW592223 461 bp mRNA EST 22-MAR-2000 hf41a01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934408 3', mRNA sequence.
                                                                                                                                                                                                                                                        110 GIGATICCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGA
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Pred. No. 1.8e-123;
0; Mismatches 4;
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/db xref="taxon:9606"
/db xref="taxon:9408"
/clone=lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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125 c 114 g 129 t
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Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW592223.1 GI:7279399
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Unpublished (1997)
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Best Local Similarity 99.1
Matches 455; Conservative
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TITLE
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AGCAGAGCGT 349
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 501)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C. Clayton, R.A., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Marmaros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
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                                                                                                                                                                                                                                                                                            2502 ccacaggccaagaaggtcagagccagtgaagatctgggagaccctgaactcagaaggct 2561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 GCCAGGAGGCTGCCACACGGAAGCAAGCAGATGAACTAATTTCATTTCAAGGCAGTTTTTT
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EST182568 Jurkat T-cells VI Homo sapiens CDNA 5' end, mRNA
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                                                                                                                                                                                                                               Score 253; DB 11; Length 479; Pred. No. 2.1e-122; 0; Mismatches 4; Indels
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AA311855
AA311855.1 GI:1964184
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ilarity 99.1%;
Conservative (
                                                                                                                                                                        127 c
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Matches 453;
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Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednartk,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Fenrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hunglun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                      Bioinformatics

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Emai: 3018699056
Emai: arkerlavetigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primeT: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 250; DB 5; Length 501; 100.0%; Pred. No. 8.1e-121; tive 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/db_xref="ATCC (inhost):159063"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Si
Xho!"
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Z17886.1 GI:30720
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Matches 250; Conservative
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                     Bonaldo, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 299)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,A.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessiar,A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ws18c04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2497542 3' similar to SW:YATA_SCHPO Q10155 HYPOTHETICAL 90.6 KD PROTEIN C104.10 IN CHROMOSOME I. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 aggatgaaaccatgacagtttaccagatccccatacacagtgaacagaggagaaagc 630
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library. Cloning vector pBluescript SK(+)"
77 c 70 g 56 t
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/clone_lib="Stratagene cDNA library Human heart,
cat#936208"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 248; DB 147; Length 299; 99.7%; Pred. No. 9e-120;
                                                                                                                                     and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
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                                                                                                                                                                                      Contact: Genzentrum Muenchen
Laboratorium fuer molekulare Biologie
Am Klopferspitz 18a,8033 Martinsried,Germany
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                                                                                                                                                                                                                                        Email: obermaier@vms.biochem.mpg.de
                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:DOS7384E"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                          Location/Qualifiers
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Unpublished (1997)
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGSP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 625 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library Nor_CGAP_GG4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made 1160m the same library (clonelDs 1257096-1258631, 1469064-1470983, and 1475592-1476743), subtraction by Bento Soares and M. Fatima Bonaldo.
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InMAGE:2497542"
/clone=lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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Best Local Similarity 100.0%; Pred. No. 3.1e-119;
Matches 247; Conservative 0; Mismatches 0;
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Query Match
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Corganism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="TN0060"

/dev_stage="Adult"

/note="organ: testis_normal; Vector: puc18; Site_1: Smal;

/note="organ: testis_normal; Site_1: Smal; Site_1: Smal;

/note="organ: testis_normal; Site_1: Smal; Site_1: Smal;

/note="organ: testis_normal; Site_1: Smal; Site_1: Smal; Site_1: Smal;

/note="organ: testis_normal; Site_1: Smal; Site_1: Smal; Site_1: Smal; Site_1: Smal;

/note="organ: testis_normal; Site_1: Smal; Si
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=CM4-TN0060-290
Seq primer: puc 18 forward
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                       Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                        Simpson, A.J.
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AUTHORS
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information can be
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
oe91f04.s1 NCI_CGAP_CO12 Homo sapiens cDNA clone IMAGE:1419007,
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Tel: (301) 496-1550

Tel: (301) 496-1550

Tel: (302) 496-1550

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Inc.

Clone distribution: NOI-CGAP clone distribution informatic found through the I.M.A.G.E. Consortium/LINL at:

www-blo.llnl.gov/Dbrp/image/image/image.html

Insert Length: 1787 std Error: 0.00

Seq primar: -40ml3 fwd. Er from Amersham

High quality sequence stop: 375.

Location/Qualifiers
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ilarity 99.5%; Pred. No. 3.6e-118;
Conservative 0; Mismatches 1;
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/clone="IMAGE:1419007"
/clone_lib="NCI_GGAP_Col2"
                                                                                                                                                   AA838624.1 GI:2913423
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Unpublished (1997)
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/db_xref="taxon:9606"
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/dev_andult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products No. 196,716 - Budwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-NT0029-240 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-NT0029-240 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-NT0029-240 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-NT0029-240 High quality sequence start: 12 High quality sequence stop: 310.
Location/Qualifiers
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Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 346)
Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                      AW889463 346 bp mRNA EST 24-MAY-2000
RCG-NT0029-240400-011-B07 NT0029 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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Fax: +55-11-2707001
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H22087 414 bp mRNA EST 06-JUL-1995 3734c04.rI Soazes breast 3NbHBSt Homo saplens cDNA clone IMAGE:160134 5' similar to SP: KK59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC ', mRNA sequence.
                                            96
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Bonaldo." 107 c 100 q 109 t 5 others
2009 ggtgcacacctctggctggaaagtggtctattccggggacaccatgccctgcgaggctct
                                    Score 238; DB 141; Length 414; Pred. No. 1.8e-114;
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/db_xref="taxon:9606"
/clone="IMAGE:160134"
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Conservative
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Matches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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KEYWORDS
SOURCE
ORGANISM
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AI201492/c
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ORIGIN
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AUTHORS
TITLE
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                                                                                                                                                                                                                                   152
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/tissue_type="choriocarcinoma"
/lab_host="MIE_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="MIE_MGC_21"
/note="Organ: placenta; vector: poTB7: Site_1: XhoI;
/note="Organ: placenta; vector: poTB7: Site_1: XhoI;
/note="Organ: placenta; vector: poTB7: Site_1: XhoI;
/note="Organ: placenta; vector: poTB7: Site_2: EcoRI; cDNA made by oliqo-dT priming.
/note="Organ: placenta; vector: poTB7 cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(6). Size-selected 550bp
/for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
/stratagene) and Superscript II RT (Life Technologies)."
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM31 row: p column: 09 High quality sequence start: 4 High quality sequence stop: 615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE409312 691 bp mRNA EST 21-JUL-2000 601300940F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635576 5'
                                                                                                                                                                                                                                                             289 AACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAAGTTAAAGGTTGCTCGCCTG 230
                                                                                                                                         gacaacatattcctgacacgaatgcactggtctaatgttgggggcttaatgtggaatgatt 425
                                                                                                                                                                                       229 GACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGGCTTAAGTGGAATGATT 170
                                                                                                                                                                                                                                     426 cttactttaaaggaaaccgggcttccaaagtgtgtactttctggacctccacaactggaa 485
                                                                                                                                                                                                                                                                                                                               486 aaatacctcgaagcaatcaaaatatttctggtccattgaaaggaatagaactggctgtg 545
  Gaps
                                                                                                                                                                                                                                                                                                                                                       109 AAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTG
                                                  aactgtggagaaggcgttcagagactcatgcaggagcacaagttaaaggttgctcgcctg
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                        546 eggececactetgececagaatacgaggatgaaaceatgaeagtttaee 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                49 CGCCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTTTACC 1
    Indels
    ;
    Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:3635576"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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    Conservative
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    288;
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TERSION
SYWORDS
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    Matches
                                                                                                                                              366
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.s409312
.ocus
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/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-98679, 1101192-1101959, and 1217928-1220515).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
a 119 c 109 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 30-OCT-1998 sapiens cDNA clone IMAGE:1943789 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 439)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 GGACCCGCTGCGGCACCTGCGCACGCGAGAGCGCGGGACCGTCGGGGTGCTCCGGCGG 203
                                                                                                                                                                                         ggacccgctgcgcacctgcgcacgcgagagagcgcggaccgtcggggtgctccggcgg 211
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                           24 TITIGGTGGAGACGGCGCATGTGGCGCCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACG 83
93
                                                                                                                                                                                                                                                                                    cccaaacaccgtgtacctgcaggtggtggcagcgggtagccgggactcgggcgccg 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1943789"
/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI201492 439 bp mRNA
qs74b03.x1 NCI_CGAP_Pr28 HOMO
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Insert Length: 717 Std Erro
Seq primer: -400F from Gibco
High quality sequence stop: 4
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI201492.1 GI:3754098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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Best Local Similarity
Matches' 435; Conserv
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8.0%; Score 236; DB 107; Length 691; 100.0%; Pred. No. 2.2e-113;

Query Match Best Local Similarity

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Similarity
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                                                                                                                                                                                                                                                                                                              human.
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ORIGIN
                                                                                                                                                                                  RESULT 77
H14462/c
                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
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AUTHORS
                                                                                                         406
                                                                                                                                      53
                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 233)
Ye,Z. and Connor,J.R.
Identification of Iron Regulated Genes by Rescreening cDNA
Libraries from SSH with Antisense Probe from Three Iron Conditions
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF188525 233 bp mRNA EST 02-MAR-2000 AF188525 Homo sapiens ATCC HTB-12; SW1088 Homo sapiens cDNA clone INIG 1, mRNA sequence. AF188525 GI:7144571
                                                             2697
                                                                                                                                                                                   2817
                                                                                                                                                                                                                                                                                                         2878 agagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtatttcagctg 2937
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                                                                                                                    286 agttcaaccggtatctcttcaactgtggagaaggcgttcagagactcatgcaggagcaca 345
                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                           Neuroscience and Anatomy
Pennsylvania State University College of Medicine
500 University Drive, Hershey, PA 17033, USA
library screened by SSH and reverse Northern blot; decreased
expression in iron loading was confirmed by Northern blot.
Location/Qualifiers
2578 acgcacgcaccgtatctgccctccttgctggtagaagctgaagagcacggtccccagg
                379 ACGCACGCACCGTATCTGCCTTCCTTGCTGGTAGAAGCTGAAGAGGACGGTCCCCCAGG
                                                           2638 aggcagctcaggataggtggtatggagctgtgccgaggcttgggctcccacataagcact
                                                                                                                                                                                     acggaagcaagcagatgaactaatttcatttcaaggcagtttttaaagaagtcttggaaa
                                                                                                                                                                                                                                                               139 CAGACGCGCACCTTTCCTCTAATCCAGCAAATGATTCCCTGCACACAGAGACAAGC
                                                                                         319 AGGCAGCTCAGGATAGGTGTATGGAGCTGTGCCGAGGCTTGGGGTCCCACATAAGCACT
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/clone=IRIG 1"
/clone=Lipe="Homo sapiens ATCC HTB-12; SW1088"
/tissue_type="astrocytoma"
/cell_line="ATCC HTB-12; SW1088"
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7.8e-112;
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100.0%; Pred. No. /...
0; Mismatches
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.9
Best Local Similarity 100.
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Ye Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
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High quality sequence stops: 268
Source: IMAGE Consortium, LLNL
This clone is available through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 509 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 268.
High quality sequence stop: 268.

Location/Qualifiers
I. #394

/ Ap_xref="Robe:578182"

/ Ab_xref="Robe:578182"

/ Ab_xref="Robe:578182"

/ Clone="Laxon:9606"

/ Clone="Liba" Soares breast 3NbHBst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 394)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikih,L., Rohlifing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot
                                                            Gaps
                                                                                                                                                                                                                                                                                                             394 bp mRNA EST 27-JUN-1995
Soares breast 3NbHBst Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20. Library constructed by Bento Soares and M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. '8.1e-112;
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yl25f04.rl Soares breast 3NbHBs1
IMAGE:159295 5', mRNA sequence.
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Tumor Gene Index
Unpublished (1997)
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 865)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                              AA522537 865 bp mRNA EST 20-AUG-1997 ni38e08.sl NCI_CGAP_Lul Homo sapiens cDNA clone IMAGE:979142 3'
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                                                        gattettaetttaaaggaaacegggetteeaaagtgtgtaetttetggaeeteeaeaet 481
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               233 CCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGCTTAAGTGGAAT 174
                                                                                     173 GATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACT 114
                                                                                                                                              54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (302) 496-1550
Tel: Cobert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                          7.8%; Score 232; DB 8; Length 865; llarity 99.5%; Pred. No. 2.9e-111; Conservative 0; Mismatches 1; Indels
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www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 436.
Location/Qualifiers
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227 g 218 t
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/db_xref="taxon:9606"
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235 c 22
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Matches 402;
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLone distribution: NGI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 846 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 255.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 282)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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om75b03.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552973
mRNA sequence.
AA928608
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                                                                                       343 TCCTTGCTGGTAGAAGAGGTGAAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/clone="IMAGE:1552973"
/clone_lib="NCI_CGAP_GC4"
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/lab_host="DH10B"
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I (Dases 1 to 202)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Kilmek, K.M., Kelley, J.C., Liu, L.T., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weiden, J.C., Liu, L., Musch, D.F., Peng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Huj, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weiter, Rosen, C.M., and
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Initial Assessment of Human Gene Diversity and Expression Patterns
assed Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)
96026280
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For clone availability, additional sequence and expression
information related to this EST, please contact the TiGR Database
(tdbinfoetdb.tigr.org)
Seq primer: Mi3 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 bp mRNA EST 06-SEP-1995
Human White blood cells Homo sapiens CDNA 5' end similar
                                                                                              2790 aaggcagtttttaaagaagtcttggaaacagacggcggcacctttcctctaatccagcaa 2849
                                                                                                                    168 AAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTCCTCTAATCCAGCAA 109
                                                                                                                                                                                                                                                                                    108 AGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCG 49
                                                                                                                                                                                                                                                            2850 agtgattccctgcacaccagagacaagcagagtaacaggatcagtgggtctaagtgtccg
             Length 282;
                                                                                                                                                                                                                                                                                                                                           Score 228; DB 13; I
Pred. No. 3.5e-109;
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/organism="Homo sapiens"
/db_xref="ATCC (inhost):104694"
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699956
Fax: 3018699423
7.7%; Scor.
100.0%; Pred. No. 3...
... 0; Mismatches
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T34024.1 GI:616122
                                                  Conservative
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                              Best Local Similarity
Matches 228; Conserv
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EST61387 B
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               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., Ph.D., CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WOI-CGAP clone distribution, information can found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                              1672 ctgtgtttgtgtcccacctgcacgcagatcaccacagggcttgccaagtatcttgctgc 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1732 agagagaacgcgccttggcatctttgggaaagccgcttcaccctttgctggtggttgccc 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1792 ccaaccagctcaaagcctggctccagcagtaccacaaccagtgccaggaggtcctgcacc 1851
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                                                                                                                                                                                                                              Length 282;
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/db_xref="taxon:9606"
/clone_lib="Human White blood cells"
/tissue_type="white blood cells"
/note="Organ: blood"
a 83 c 73 g 62 t 2 of
                                                                                                                                                                                                                           7.7%; Score 228; DB 145;
100.0%; Pred. No. 3.5e-109;
tive 0; Mismatches 0;
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Insert Length: 2467 Std Error: 0.00
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/db_xref="taxon:9606"
/clone-"IMAGE:1980109"
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High quality sequence stop: 397
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Unpublished (1997)
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AI357786
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Query Match
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COMMENT
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KEYWORDS
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National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausberg(anih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gatcagtgggtctaagtgtccgagacttaacgaaaatagtatttcagctgcaataaagat 2947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE615669 872 bp mRNA EST 24-AUG-2000 601279347F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611338 5'
                                                                                                                                  2768 gcagatgaactaatttcatttcaaggcagtttttaaagaagtcttggaaacagacggcgg 2827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cacettteetetaatecageaagtgatteeetgeacaceagagaeaageagagtaaeag 2887
                                                                                                                                                                                                                                                                     ggataggtggtatggagctgtgccgaggcttgggctcccacataagcactagtctataga 2707
                                                                                                                                                                                                                                                                                                                                        tgeetettaggaetggtgeetggeacageegegggeeaggaggetgeeacaeggaageaa 2767
                                                                                                                                                                                                    TGCCTCTTAGGACTGGTGCCTGGCACAGCTGCGGGCCAGGAGGCTGCCACACACGGAAGCAA 194
                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 GATCAGIGGGICIAAGIGICCGAGACIIAACGAAAAIAGIAIIICAGCIGCAAIAAAGAI 14
                                                                                                                                                                                                                                                                                       313 GGATAGGTGGTATGGAGCTGTGCCGAGGCTTGGGGCTCCCACATAAGCACTAGTCTATAGA
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                                                               Length 433;
                                                                                                  Indels
                                                                 Score 227; DB 19;
Pred. No. 1.2e-108;
                                                                                                  0; Mismatches
119
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Plate: LLCM268 row: n column: 11
High quality sequence stop: 667.
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/db_xref="taxon:9606"
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BE615669.1 GI:9897268
                                                                 7.7%;
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117
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                                                                                  Similarity
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Best Local &
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AUTHORS
TITLE
JOURNAL
ASE COUNT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 291)
2 (Bish W. Hawkins M., Eukor, M., Le, M., Le, N., Mardis, E., Moore M. M., Mardis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor NbHOT Homo sapiens cDNA clone to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8 INTERGENIC REGION. ;, mRNA sequence.
/tissue_type="ademocarcinoma"
//lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; vector: pOTB7; Site_1: XhO1;
Site_2: EccNI; cDNA made by oligo-dT priming.
Directionally cloned into EccNIXhoI sites using the following S' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.ilnl.gov) for further information. Possible reversed clone: similarity on wrong strand possible reversed clone: poly not found insert Length: 1829 std Brror: 0.00 Seq primer: -1819 Std Brror: 0.00 High quality sequence stop: 271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                             Length 872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 224; DB 110;
Pred. No. 5e-107;
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                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. .v. +ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 224;
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Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                      257
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zt29911.s1 Soares ovary
IMAGE:723812 3' similar
KD PROTEIN IN SIS2-MTD1
                                                                                                                                                                                                                                                         Technologies)
239 c
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 224; Conservative
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/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polyluher; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and so
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
tens; DNA was used as tracer in a subtractive hybridization
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
subtraction by Bento Soares and M. Fatima Bonaldo. "
a 130 c 120 g 133 t lothers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 228)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 CATITICAAGGCAGTITITAAAGAAGTCATGGAAACAGACGGCGGCGCCCTTTCCTCTAATC 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 CAGCAAAATGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  7.4%; Score 220; DB 25;
98.9%; Pred. No. 6.3e-105;
tive 0; Mismatches 5;
                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2253699"
/clone_lib="NCI_CGAP_Pr28"
 High quality sequence stop: 458 Location/Qualifiers
                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                               /sex="male"
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Matches 470; Conservative
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                                           source
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Email: Robert_Strausbergenih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Prayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 876 Std Error: 0.00
Seq primer: -40UP from Gibco
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tu42d02.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253699 3',
mRNA sequence.
AI804749 GI:5370221
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 catatteetgaeacgaatgeaetggtetaatgttgggggettaagtggaatgattettae 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 ccgggactcgggcgcgctctacgtcttctccgagttcaaccggtatcttctaactg 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 tggagaaggcgttcagagactcatgcaggagcacaagttaaaggttgctcgcctggacaa 370
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:723812"
/clone_11b="Soares ovary tumor NDHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 221; DB 4; Le
100.0%; Pred. No. 1.8e-105;
tive 0; Mismatches 0;
Location/Qualifiers
                                                                                                             /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0
Matches 221; Conservative
                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human,
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 440)

1 (lases I to 440)

M., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Roblifing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, T.R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 365
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity on wrong strand
Forsible reversed clone: similarity on using strand
Forsible reversed clone: similarity sound
Forsible reversed clone: similarity sound
Forsible reversed clone: similarity sound
Seq primer: ml3 -40 forward
High quality sequence stop: 365.
                                                                                                                                                                                                                                                                                                                        N36229 448 bp mRNA EST 16-JAN-1996
yy30c04.sl Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:272742 3' similar to SW:YK59_YEAST P36159 HYPOTHETICAL 96.8
KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION. [1] ;, mRNA sequence.
       121 GGCGCCGCGCTCTACGTCTTCTCCGAGTTCAACCGGTATCTCTTCAACTGTGGAGAAGGC 180
                                                                                                                       181 GTTCAGAGACTCATGCAGGAGCACAAGTTAAAGGTTGC 218
                                                                          321 gttcagagactcatgcaggagcacaagttaaaggttgc 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N36229.1 GI:1157371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
Contact: Wilson RK
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N36229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Glone_lib="NCI_CGAP_Sub6"
//lab_lost="Planting (Life Technologies)" with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; NCI_CGAP_Sub6
is a subtracted library derived from BW, which consists of
a mixture of four normalized libraries: NCI_CGAP_Bun50,
NCI_CGAP_Lul3, NCI_CGAP_Ov18, GBC1. The NCI_CGAP_Bun50,
NCI_CGAP_Lul3, NCI_CGAP_Ov18, GBC1. The NCI_CGAP_Bun50,
NCI_CGAP_Lul3, NCI_CGAP_CV18, GBC1. The NCI_CGAP_Bun50,
NCI_CGAP_Kid3 pool 1 LLAM 334-337, 3682-3683,
3798-3803 (Image CloneIDS 1323911,
1456008-1466775_1500552-1502855); NCI_CGAP_Kid5 pool 1
LLAM 338-3342,3722-3725, 3776-3778 (Image CloneIDS
1323912-132581, 147158-147290; 1429104-14292355);
NCI_CGAP_Lu5 pool 1 LLAM 2457-2459, 2758-2759,
NCI_CGAP_Lu5 pool 1 LLAM 2457-2459, 2758-2759,
3062-3068 (Image CloneIDS 985608-986759, 1101192-1101959,
1217928-1220615); NCI_CGAP_CO10 pool 1 LLAM 2457-2459,
3062-3068 (Image CloneIDS 985608-986759, 1101192-1101959,
1217928-1220615); NCI_CGAP_CO10 pool 1 LLAM 2457-2459,
3062-3068 (Image CloneIDS 985608-986759, 1101192-1101958,
310816-2710535) and NCI_CGAP_Sub2 (Image CloneIDS 27105155) and NCI_CGAP_Sub2 (Image CloneIDS 27105155) and NCI_CGAP_Sub2 (Image CloneIDS 27105155) and NCI_CGAP_Sub2 (Image CloneIDS 2710555) and NCI_CGAP_Sub2 (Image CloneIDS 27105
                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
11s likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: Mi3 Forward
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Matches 218; Conserv
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                                                                                                                                                                                                            double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                           Length 448;
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                                                       /clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                           7.4%; Score 218; DB 142;
ilarity 100.0%; Pred. No. 7.2e-104;
Conservative 0; Mismatches 0;
                                                                                                          /tissue_type="melanocyte
/organism="Homo sapien:
/db_xref="GDB:3882384"
/db_xref="taxon:9606"
/clone="IMAGE:272742"
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 218;
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ggcgcgcgctctacgtcttctccgagttcaaccggtatcttcaactgtggagaaggc 320

261

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145 TGGAAACAGACGGCGCACCTTTCCTCAATCCAGCAAAGTGATTCCCTGCACACAGAG 86
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AW247380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 239.
Location/Qualifiers
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                                                                                                                                                                                                                                                                        AW511765 316 bp mRNA EST 03-MAR-2000 xu76f03.xl NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807645 3',
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 316)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue-Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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                                                                   372 atattoctgacacgaatgcactggtctaatgttgggggcttaagtggaatgattcttact
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/clone="INAGE:2807645"
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/tissue_rype="renal_cell_tumor"
/lab_host="DH108"
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Pest Local Similarity 99.6%; Pred. No. 9.3e-102;
Matches 264; Conservative 0; Mismatches 1;
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AW511765
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Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Barkeley MGC Sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/Dbrp/image/image.html Base Calling / Quality Scores: PRED from University of Washingtion Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophina Genome Project. University of Washingtion Genome Center: http://www.genome.washington.edu plate: LLCM4 row: L. column: 17 High quality sequence stop: 225.
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="Inba"NIH_MGC_1"
/clone=Lib="NNIH_MGC_2"
/clone_Lip="MGC_2"
/clone_Lip="MGC_3"
/lab_host="DH10B (Phage-resistant)"
/note="Organ: lung: Vector: porB7; Site_l: xhol: Site_2:
CorRI: CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/Xhol sites using, the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
callifornia, Berkeley) using zah-conA synthesis, kit
(Stratagene) and Superscript II RT (Life Technologies)."
39 a 83 c 94 g 33 t
                                                                                                                                                                                                                                                                                                                                                        AW247380 249 bp mRNA EST 07-JAN-2000 2820640.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820640 5', mRNA sequence.
AW247380.1 GI:6590373
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2872 acaagcagagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtattt 2931
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100.0%; Pred. No. 3.6e-100;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onpublished (1999)
Other ESTs: 2820640.3prime
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg (annual povent)
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                                                                                                                                                                 CAGCTGCAATAAAGATTGAGTTTGC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-HT0217-201199-022-h08&t3=1999-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 74.
                                                                                                                                                                                                                                                                                            AW378247 650 bp mRNA EST 04-FEB-2000
RC1-HT0217-201199-022-h08 HT0217 Homo sapiens CDNA, mRNA sequence.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2291 tgaccacatgaaggtctgctttggagactttccaacaatgcccaagctgattcccccact 2350
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                                                                           121 aggcacccgcccgccgcgagcggccgcgcaaggacccgctgcggcacctgcgcacgcgag 180
tttgctcgctgctgcggtccgcgggccggacgcaccatgtcgcagggacgcaccatatcgc 120
                                    80 TTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACATGTCGCAGGGACGCACCATATCGC 139
                                                                                                 140 AGGCACCGCCGCCGCGCGGCGCGCGCAAGGACCCGCTGCGGCACCTGCGCAAGGAC
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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ilarity 100.0%; Pred. No. 4.3e-99;
Conservative 0; Mismatches 0;
                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0217"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                   AW378247.1 GI:6882906
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 219)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                AASO4146 219 bp mRNA EST 18-AUG-1997
aa59e06.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825250 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA, Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2752 'tgocacacggaagcaagcagatgaactaatttcatttcaaggcagtttttaaagaagtct 2811
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consorttum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 175.
Locatiod/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //tissue_type="germinal center B cell"
//lab_host="DH10B"
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/organism="Homo sapiens"
                                          /db_xref="taxon:9606"
/clone="IMAGE:825250"
/clone_lib="NCI_CGAP_C
                                                                                                                                                                                                                                                                      AA504146
AA504146.1 GI:2240306
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Unpublished (1997)
                                                                                                                                                                                                                                                      mRNA seguence.
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REFERENCE AUTHORS TITLE JOURNAL 'OMMENT

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Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Eukaryota: Metazoa; Chordata; Cararhini; Hominidae; Homo.

La (bases 1 to 472)

La (bases 1 to 472)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washlowerck EST Project
Unpublished (1995)

Contact: Wilson RK
Washington University School of Medicine
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 327
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R51138 472 bp mRNA EST 18-MAY-1995 yq71c08.r1 Soares infant brain INIB Homo saptens cDNA clone IMAGE:38752 5' similar to SP:YK59_YEAST P36159 HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-WID1 INTERGENIC ; mRNA sequence.
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
1: Site_2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5 AACTGGAAGAATTCTTTTTTTTTTTT 3'];
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                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                          tcactcatgaaggaagagattttggctgaagagctgtgtactcctccagatctggtg
                                                                                                                                                                                                                                                                                                                                                                                                          151 CIGCITITIGIGGIGGIAGAAIGICCAGAIGAAGCITCAITCAACCCAICIGGAGAAIG
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/clone_lib="Soares infant brain INIB"
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/db_xref="GDB:411293"
/db_xref="taxon:9606"
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High quality sequence stop: 327
Location/Qualifiers
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/note="Organ: parathyroid gland; Vector: p1713D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 678 Std Error: 0.00
Seq primer: mob.REGA+ET.
Location/Qualifiers
                                                                                                2872 acaagcagagtaacaggatcagtgggtctaagtgtccgagacttaacgaaaatagtattt 2931
     159 TGGAAACAGACGGCGCACCTTTCCTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAG 100
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'tissue_type="parathyroid tumor'dev_stage="adult"
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/db_xref="GDB:1259575"
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Contact: Wilson RK
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Query Match Best Local Similarity

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BASE COUNT

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Homo sapiens
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qa46h05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1689849
3', mRNA sequence.
AI141263
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
                                 1550 tgccacacttgtcaacataagccccgacacgtctctgctactggactgtggtgagggcac 1609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Imail: Nobert_Strausbergeinh.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 71 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 233.
Location/Qualifiers
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Pred. No. 2.8e-93;
0; Mismatches. 4;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IXAAGE:1.68949"
/clone_11b="Soares_NhHMPu_S1"
Mismatches
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Unpublished (1997)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhin; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 394)

8 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

9 C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White,

9 C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White,

9 C.J., Lee, N.H., Kirkness, E.F., Medistock, R.G., Gocayne, J.D., White,

10 C.L., Hand, D.C., Earle-Hughes, J., Fine, L.D., Fitzgerald,

11 M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

12 Kalley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

13 Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

14 Moreno-Palanques, R.E., Scott, J.L., Saudek, D.M., Shirley, R.,

15 Sands, D., Fong, D.-F., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

16 Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

17 Mu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

18 Kunsch, C., Hangjun, J., Li, H., Waissner, P.S., Olsen, H., Raymond, L.,

18 W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and

19 Venter, J.C.
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Initial assessment of human gene diversity and expression patterns
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9712 Medical Center Drive, Rockville, MD 20850 USA.
9712 Medical Center Drive, Rockville, MD 20850 USA.
9713 Medical Center Drive, Rockville, MD 20850 USA.
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
email: arkerlav@tigr.org
information related to this EST, please check the TiGR Human Gene Ingex (http://www.tigr.org/tdb/hgi/hgi.html)
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EST52407 Greater omentum IV Homo sapiens cDNA 5' end, mRNA
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                                                                                                                tgaagagcacggtcccccaggaggcagctcaggataggtggtatggagctgtgccgaggc
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1 (Dases 1 to 276)

1 (Dases 1 to 276)

2 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult C.J., Lee, N.H., Kirknes; E.F., Weinstock, K.G., Gocayne, J.D., White C.J., Lee, N.H., Kirknes; E.F., Weinstock, K.G., Gocayne, J.D., White C.J., Lee, N.H., Kirknes; E.F., Weinstock, R.G., Gocayne, J.D., White C.J., Eltzhudh, M.M., Eritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Glodek, A., Gnehm, C.L., Liu, L.-I., Marmaros; S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.R., Collins, E.J., Li, Kunsch, C., Hustings, G.A., He, W.W., Kunsch, C., Husting, J., Xu, C., Yu, G.L., Kuben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and
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Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA378232 276 bp mRNA EST 21-APR-1997
EST90926 Synovial sarcoma Homo sapiens CDNA 5' end, mRNA sequence.
AA378232
                                                                         /db_xref="ATCC (inhost):147767"
/db_xref="taxon:9606"
/clone_lib="Greater omentum IV"
/dev_stage="adult"
/note="Organ: omentum; Vector: pBluescript SK-; Site_l:
ECORI; Site_2: XhoI"
108 c 108 g 96 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1683 tcccacctgcacgcagatcaccacacgggcttgccaagtatcttgctgcagagagaacgc 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 TCCCACCTGCACGCAGATCACCACACGGCTTGCCAAGTATCTTGCTGCAGAGGAACGC 136
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0
                                                                                                                                                                                                                                                                                       Length 394;
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9712 Medical Center Drive, Rockville, MD 20850 USA
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                                                                                                                                                                                                                                                                                       Query Match 6.5%; Score 193; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.3e-90;
Matches 193; Conservative 0; Mismatches 0;
               Location/Qualifiers
1. 394
/organism="Homo sapiens"
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Seq primer: M13 Reverse.
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Fax: 3018699423
Email: arkerlavetigr.org
Email: arkerlavetigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
seq primer: M13 Reverse.
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1 (bases 1 to 290)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                  /tissue_type="synovial membrane"
/dev_stage="adult, 20 yrs"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2011 tgcacacctctggctggaaagtggtctattccgggggacaccatgcctgcgaggctctgg 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2071 tecggatggggaaagatgeeacetectgatacatgaageeaceetggaagatggtttgg 2130
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Genethon Centre de recherche sur le Genome Humain
1, rue de 1/Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         others
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                                                                                                                                                       Location/Qualifiers
1. 276
/organism="Homo sapiens"
/db_xref="ATCC (inhost):182644"
/db_xref="taxon:9606"
/clone_lib="Synovial sarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 184; DB 6;
Pred. No. 7.2e-86;
0; Mismatches 1.
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Single read.
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Best Local Similarity 99.6%;
Matches 234; Conservative
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                                                                                                                                              /tissue_twpe="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="corpan: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female: dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain;
cloned solato-drip primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press" 3 others
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Hobses 1 to 424)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., R., Williamson,A., Wohldmann,P. and Wilson,R. Trevaskis,E., Waterston The WashUrNerck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High qality sequence stops: 315
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 TITCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTGGTTCACATGGCCCCA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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yj47e10.s1 Soares placenta Nb2HP Homo sapiens CDNA clone
IMAGE:151914 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1026 tttcagaggtaccaaggaaaggcagatgccccgtggccttggtggttcacatggcccca
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 290;
                                                                                      /clone="c-23e06"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 182; DB 147;
100.0%; Pred. No. 8.3e-85;
tive 0; Mismatches 0;
                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
Seq primer: (-21)M13_universal.
Location/Qualifiers
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H03318.1 GI:866251
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Best Local Similarity 100.(
Matches 182; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 482)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project; (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL : contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 749 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 455.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.2%; Score 182; DB 141;
Best Local Similarity 100.0%; Pred. No. 8.5e-85;
Matches 182; Conservative 0; Mismatches 0;
Std Error: 0.00
                                                                                    1. .424
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Insert Length: 1152 Std Error:
Seq primer: Promega - 21m13
High quality sequence stop: 315.
Location/Qualifiers
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T72963.1 GI:689638
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2562 gtgtgtcttctgccccacgcacgcacccgtatctgccctccttgctggtagaagctgaag 2621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2622 agcacggtcccccaggaggcagctcaggataggtggtatggagctgtgccgaggcttggg 2681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EE519874 577 bp mRNA EST 24-AUG-2000 601473130T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876223 3' EE519874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD_TP_Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov: k column: 08
Plate: LLCM623 row: k column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                    2502 ccacaggccaagaaggtcagagcccagtgaagatctgggagaccctgaactcagaaggct 2561
                                                                                                                                                                                                                                                                                                                                                                                                                                     456 CCACAGGCCAAGAAGGTCAGAGCCCAGTGAAAATCTGGGAGACCCTGAACTCAGAAGGCT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 GIGIGICITCICCCCCACGCACGCACCCGTAICIGCCCTCCTIGCIGGTAGAAGCIGAAG
                                                        /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                     6.1%; Score 180; DB 15; Length 482;
100.0%; Pred. No. 9.9e-84;
tive 0; Mismatches 0; Indels
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            /organism≂"Homo sapiens"
/db_xref="taxon:9606"
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/clone="IMAGE:3876223"
                                          /clone="IMAGE:1655159"
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Matches 180; Conserv
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

In (bases 1 to 376)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,M., Hawkins

M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E.,

Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,

Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Maira,M.

Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High qality sequence stops: 335 Source: IMAGE Consortium; LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 954 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                               ö
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/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Insert size 1.8 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                2654 giggialggagcigigccgaggcitgggciccacalaagcaciagtcialagaigccic 2713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          re55b06.rl Stratagene liver (#937224) Homo sapiens cDNA clone PMAGE:85523 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 GIGGIAIGGAGCIGIGCCGAGGCITGGGCTCCCACATAAGCACTAGICTATAGATGCCTC
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                           Length 577;
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/lab_host="SOLR cells (kanamycin resistant)
                                                                                                                                                                                                                                                                                                                                                                  Indels
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/sex="male"
                                                                                                                                                                                                                                                                                                        6.1%; Score 179; DB 110;
100.0%; Pred. No. 3.4e-83;
tive 0; Mismatches 0;
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/db_xref="GDB:502580"
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High quality sequence stop: 335
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Insert Size: 954
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                                                                                                                                                                     Technologies.
189 c
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/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
; Site_2: XhOI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-Zap XR Vector; -5' adaptor sequence: 5'
GAATTGGGANGAG 3' -3' adaptor sequence: 5'
CTGGAGTTTTTTTTTTTTTTTTTTTTTTTTT 3'"

R2 a 94 c 121 g 63 t 16 others
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.ob time: 14671 sec